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OM protein - protein search, using sw model

Run on: November 3, 2005, 20:38:14 ; Search time 165 Seconds
(without alignments)
1172.001 Million cell updates/sec

Title: US-09-918-715-230

Perfect score: 2691

Sequence: 1 MRGELMLVLVLRRAARALS.....YAEVPSGHEKGFMEAEQC 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2691	100.0	500	5 ABB90749	Abb90749 Human Tum
2	2691	100.0	500	6 ABUS4456	Abu54456 Human Tum
3	2691	100.0	500	7 ADI21063	Adi21063 Novel hum
4	2691	100.0	500	8 ADH13230	Adh13230 Human mal
5	2691	100.0	527	7 ADI21554	Adi21554 Novel hum
6	2691	100.0	527	7 ADI21553	Adi21553 Novel hum
7	2691	100.0	1002	5 ABB90723	Abb90723 Human Tum
8	2691	100.0	1002	6 ABUS4430	Abu54430 Human Tum
9	2607	96.9	488	7 ADI21064	Adi21064 Novel hum
10	2209	82.1	500	5 ABB90783	Abb90783 Mouse Tum
11	2209	82.1	500	5 ABB90729	Abb90729 Mouse Tum
12	2209	82.1	500	6 ABUS4436	Abu54436 Mouse Tum
13	2209	82.1	500	6 ABUS4490	Abu54490 Mouse Tum
14	2185	81.2	431	4 AAB85400	Aab85400 Tumour en
15	2185	81.2	431	6 AB001434	Ab001434 Human Tum
16	2007	74.6	400	3 AAB43131	Aab43131 Human ORF
17	1326	49.3	351	8 ADR09329	Adr09329 Human pro
18	1295	48.1	499	4 AAB85396	Aab85396 Stem cell
19	1295	48.1	499	6 AB001430	Ab001430 Human ste
20	1295	48.1	529	4 AAB85394	Aab85394 Stem cell
21	1295	48.1	529	5 ABB90734	Abb90734 Human Tum
22	1295	48.1	529	5 ABB90726	Abb90726 Human Tum
23	1295	48.1	529	5 ABP53349	Abp53349 Human tra
24	1295	48.1	529	5 ABG69157	Abg69157 Human ste
25	1295	48.1	529	5 ABG69161	Abg69161 Human pro

ALIGNMENTS

RESULT 1

ABB90749
ID ABB90749 standard; protein; 500 AA.

XX AC ABB90749;

DT 30-MAY-2002 (first entry)

DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 230.

XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis.

XX Homo sapiens.

XX WO200210217-A2.

XX PD 07-FEB-2002.

XX PF 01-AUG-2001; 2001WO-US024031.

XX PR 02-AUG-2000; 2000US-0222599P.

XX PR 11-AUG-2000; 2000US-0224360P.

XX PR 11-APR-2001; 2001US-0282850P.

XX (UYJO) UNIV JOHNS HOPKINS.

XX St Croix B, Kinzler KW, Vogelstein B;

XX WPI; 2002-291856/33.

XX N-PSDB; ABL92103.

XX An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial

XX marker (TEM) protein, useful for inhibiting tumor growth.

XX Claim 1; Page 206-207; 331pp; English.

XX The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic

Abu54441 Human tum
Abu54433 Human tum
Ab001436 Human ste
Aae35354 Human TEM
Adn05749 Antipsoi
Aab31211 Amino aci
Aau29259 Human PRO
Aam39068 Human POL
Aab58635 Human PRO
Abu88183 Novel hum
Abu84498 Human sec
Aab66372 Human sec
Aab65762 Human sec
Aau99702 Human sec
Aab82941 Human PRO
Abu90062 Novel hum
Aab68311 Human sec
Abu96364 Novel hum
Abu92795 Human sec

26 1295 48.1 529 6 ABUS4441
27 1295 48.1 529 6 ABUS4433
28 1295 48.1 529 6 ABO01428
29 1295 48.1 529 6 AAE35354
30 1295 48.1 529 8 AADN05749
31 1295 48.1 529 4 AAB31211
32 1294 48.1 529 4 AAB31211
33 1294 48.1 529 4 AAB31211
34 1294 48.1 529 4 AAM39068
35 1294 48.1 529 6 ABUS8635
36 1294 48.1 529 6 ABUS86183
37 1294 48.1 529 6 ABUS84498
38 1294 48.1 529 6 ABR66372
39 1294 48.1 529 6 ABR65762
40 1294 48.1 529 6 ABUS9702
41 1294 48.1 529 6 ABUS2941
42 1294 48.1 529 6 ABUS90062
43 1294 48.1 529 6 ABR68311
44 1294 48.1 529 6 ABUS96364
45 1294 48.1 529 6 ABUS2795

CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995
XX
SQ Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 5; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.2e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLRRAALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSPDR 60
Db 1 MRGELWLLVLVLRRAALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSPDR 60

Qy 61 TQLSQDLGGGTLMADTLPDNRTRVEDNHSYVSRLYGPPSPHRELWVDVAEANRSQVK 120
Db 61 TQLSQDLGGGTLMADTLPDNRTRVEDNHSYVSRLYGPPSPHRELWVDVAEANRSQVK 120

Qy 121 IHTILSNTHRQASRVLSFDPFPYGHPLRQITTIATGGFIFMGDVVHRMLTATQVAPLMA 180
Db 121 IHTILSNTHRQASRVLSFDPFPYGHPLRQITTIATGGFIFMGDVVHRMLTATQVAPLMA 180

Qy 181 NFNPGYSDNSTVYVFDNGTVFVQWHDVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 181 NFNPGYSDNSTVYVFDNGTVFVQWHDVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240

Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRSIFEVHRIELDPKVTSMASVEFTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRSIFEVHRIELDPKVTSMASVEFTP 300

Qy 301 LPTCLQHRSCDACMSSDLTFNCSCHVLRQCSGFDYRQEWMDYGCQAEGRMCDPQ 360
Db 301 LPTCLQHRSCDACMSSDLTFNCSCHVLRQCSGFDYRQEWMDYGCQAEGRMCDPQ 360

Qy 361 DEHDSASPTSPSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
Db 361 DEHDSASPTSPSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420

Qy 421 PVHLGTVIGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTVIGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480

Qy 481 YAEVEPSGHEKEGFMWAEQC 500
Db 481 YAEVEPSGHEKEGFMWAEQC 500

RESULT 2
ABUS4456
ID ABUS4456 standard; protein; 500 AA.

XX AC ABUS4456;

XX DT 12-MAR-2003 (first entry)

XX DE Human tumour endothelial marker TEM 17.

XX KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW Tumour endothelial marker; normal endothelial marker; PEM;
KW pan-endothelial marker; polycystic kidney disease; psoriasis;
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW neovascularization; immune response; cytostatic; antidiabetic;
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.

XX OS Homo sapiens.

XX FN WO200283874-A2.

XX PD 24-OCT-2002.

XX

PF 10-APR-2002; 2002WO-US008253.
XX
PR 11-APR-2001; 2001US-0282850P.
PR 06-FEB-2002; 2002US-0354262P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX
DR WPI; 2003-093016/08.
DR N-PSDB; ABX72028.
XX

XX New purified human transmembrane protein, designated as tumor endothelial
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT psoriasis.
XX

PS Disclosure; Page 221-222; 374pp; English.

XX The present invention relates to a novel method for the isolation of
CC endothelial cells (ECs), and the identification of genes expressed in
CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
CC identified in human ECs. The human EC marker proteins and the
CC polynucleotide sequences encoding them are useful for detecting,
CC diagnosing or treating tumours as well as polycystic kidney disease,
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for
CC inducing an immune response to tumour endothelial cells in a patient, or
CC for identifying candidate drugs for treating tumours. The present
CC sequence represents a human TEM or NEM protein of the invention
XX

SQ Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 6; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.2e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLRRAALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSPDR 60

Db 1 MRGELWLLVLVLRRAALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSPDR 60

Qy 61 TQLSQDLGGGTLMADTLPDNRTRVEDNHSYVSRLYGPPSPHRELWVDVAEANRSQVK 120

Db 61 TQLSQDLGGGTLMADTLPDNRTRVEDNHSYVSRLYGPPSPHRELWVDVAEANRSQVK 120

Qy 121 IHTILSNTHRQASRVLSFDPFPYGHPLRQITTIATGGFIFMGDVVHRMLTATQVAPLMA 180

Db 121 IHTILSNTHRQASRVLSFDPFPYGHPLRQITTIATGGFIFMGDVVHRMLTATQVAPLMA 180

Qy 181 NFNPGYSDNSTVYVFDNGTVFVQWHDVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240

Db 181 NFNPGYSDNSTVYVFDNGTVFVQWHDVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240

Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRSIFEVHRIELDPKVTSMASVEFTP 300

Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRSIFEVHRIELDPKVTSMASVEFTP 300

Qy 301 LPTCLQHRSCDACMSSDLTFNCSCHVLRQCSGFDYRQEWMDYGCQAEGRMCDPQ 360

Db 301 LPTCLQHRSCDACMSSDLTFNCSCHVLRQCSGFDYRQEWMDYGCQAEGRMCDPQ 360

Qy 361 DEHDSASPTSPSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420

Db 361 DEHDSASPTSPSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420

Qy 421 PVHLGTVIGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480

Db 421 PVHLGTVIGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480

Qy 481 YAEVEPSGHEKEGFMWAEQC 500

Db 481 YAEVEPSGHEKEGFMWAEQC 500

CC cytosstatic compounds through the regulation of the expression of a gene
CC or activity of a protein associated with malignant neoplasia. The method
CC is useful for prediction, diagnosis or prognosis of malignant neoplasia
CC such as breast cancer, ovarian cancer, gastric cancer, colon cancer,
CC esophageal cancer, mesenchymal cancer, bladder cancer or non-small cell
CC lung cancer. The polynucleotides and polypeptides defined in the
CC specification, antisense polynucleotides targeting the polynucleotides,
CC antibodies targeting either one of the polynucleotides or polypeptides,
CC and compounds identified by the screening methods are useful for
CC preventing or treating malignant neoplasia. The disease treated is
CC preferably breast cancer. The present sequence is that of a human
CC malignant neoplasia-related protein which may be used in the method of
CC the invention.

XX SQ Sequence 500 AA;

Query Match 100.0%; Score 2691; DB 8; Length 500;
Best Local Similarity 100.0%; Pred. No. 3.2e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELMLLVLRRAAALSPQAGHDEGPGGAAKGTVRGNRRRARESPGHVSEPD 60
Db 1 MRGELMLLVLRRAAALSPQAGHDEGPGGAAKGTVRGNRRRARESPGHVSEPD 60
Qy 61 TOLSDQLGGGTAMDITLPDNRTRVVDNHSYYSRLYGPSEPHSRELWVDVAENRSQVK 120
Db 61 TOLSDQLGGGTAMDITLPDNRTRVVDNHSYYSRLYGPSEPHSRELWVDVAENRSQVK 120
Qy 121 IHTILSNTHRQASRVLSFDFFPGHPLRQITATGFIIMGDVHRLMLTATQVAPLMA 180
Db 121 IHTILSNTHRQASRVLSFDFFPGHPLRQITATGFIIMGDVHRLMLTATQVAPLMA 180
Qy 181 NFNPYSDNSTVYFDNGTVFVQWDHVYLGQWEDKGSFTFQALHHDGRIVFAYKEIPM 240
Db 181 NFNPYSDNSTVYFDNGTVFVQWDHVYLGQWEDKGSFTFQALHHDGRIVFAYKEIPM 240
Qy 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDSPKTSMSAVEFTP 300
Db 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDSPKTSMSAVEFTP 300
Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCDPQ 360
Db 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCDPQ 360
Qy 361 DEHDASPTSFSPYDGLTFTSSSLFIDSLTTEDDTKLNYPAGDGLQNLSPKTKGT 420
Db 361 DEHDASPTSFSPYDGLTFTSSSLFIDSLTTEDDTKLNYPAGDGLQNLSPKTKGT 420
Qy 421 PVHLGTTVIGIVLAVLLVAAILAGIYINGHTSNAALFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTTVIGIVLAVLLVAAILAGIYINGHTSNAALFFIERRPHHPAMKFRSHPDHST 480
Qy 481 YAEVPSGHEKEGFMPEAEQC 500
Db 481 YAEVPSGHEKEGFMPEAEQC 500

RESULT 5

ADI21554
ID ADI21554 standard; protein; 527 AA.

XX AC ADI21554;

XX DT 15-APR-2004 (first entry)

XX DE Novel human polypeptide #33.

XX forensic; nutritional source; damaged tissue; diseased tissue;
KW myeloid cell disorder; lymphoid cell disorder;
KW bone cartilage tissue growth; tendon tissue growth;
KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;
KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.

OS Homo sapiens.

XX WO2003025148-A2.

XX PD 27-MAR-2003.

XX PF 19-SEP-2002; 2002WO-US029964.

XX PR 19-SEP-2001; 2001US-0323739P.

XX PR 13-SEP-2002; 2002US-00323739.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;
PI Haley-Vicente D;

XX WPI; 2003-354603/33.

DR N-PSDB; ADI21334.

XX New polynucleotides and secreted proteins, useful for treating myeloid or
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve
PT tissue growth or regeneration, in wound healing, and in tissue repair and
PT replacement.

XX Example 3; SEQ ID NO 805; 156pp; English.

XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide with biological activity. The polynucleotides and
CC polypeptides are useful in diagnostics, forensics, gene mapping,
CC identification of mutations responsible for genetic disorders and other
CC traits, to assess biodiversity, as nutritional sources or supplements.
CC The polynucleotides may also be used as molecular weight markers,
CC chromosome markers or map related gene positions, or as an antigen to
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are
CC useful for raising antibodies, as markers for tissues in which the
CC corresponding polypeptide is expressed, for re-engineering damaged or
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in
CC bone cartilage, tendon, ligament and/or nerve tissue growth or
CC regeneration, in wound healing, in tissue repair and replacement, in
CC healing of burns, incisions and ulcers, and in treating cancer. The
CC present sequence represents the amino acid sequence of a novel human
CC polypeptide.

XX SQ Sequence 527 AA;

Query Match 100.0%; Score 2691; DB 7; Length 527;
Best Local Similarity 100.0%; Pred. No. 3.5e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELMLLVLRRAAALSPQAGHDEGPGGAAKGTVRGNRRRARESPGHVSEPD 60
Db 28 MRGELMLLVLRRAAALSPQAGHDEGPGGAAKGTVRGNRRRARESPGHVSEPD 87
Qy 61 TOLSDQLGGGTAMDITLPDNRTRVVDNHSYYSRLYGPSEPHSRELWVDVAENRSQVK 120
Db 88 TOLSDQLGGGTAMDITLPDNRTRVVDNHSYYSRLYGPSEPHSRELWVDVAENRSQVK 147
Qy 121 IHTILSNTHRQASRVLSFDFFPGHPLRQITATGFIIMGDVHRLMLTATQVAPLMA 180
Db 148 IHTILSNTHRQASRVLSFDFFPGHPLRQITATGFIIMGDVHRLMLTATQVAPLMA 207
Qy 181 NFNPYSDNSTVYFDNGTVFVQWDHVYLGQWEDKGSFTFQALHHDGRIVFAYKEIPM 240
Db 208 NFNPYSDNSTVYFDNGTVFVQWDHVYLGQWEDKGSFTFQALHHDGRIVFAYKEIPM 267
Qy 241 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDSPKTSMSAVEFTP 300
Db 268 SVPEISSQHPVKTGLSDAFMLNPSDPVPSRRRSIFEYHRIELDSPKTSMSAVEFTP 327
Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCDPQ 360
Db 328 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCDPQ 387

QY 361 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420
 Db 388 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 447
 QY 421 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 480
 Db 448 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 507
 QY 481 YAEVPSGHEKEGFMEAEQC 500
 Db 508 YAEVPSGHEKEGFMEAEQC 527

RESULT 6

AD121553
 ID AD121553 standard; protein; 527 AA.

XX AC AD121553;

XX 15-APR-2004 (first entry)

XX Novel human polypeptide #32.

XX forensic; nutritional source; damaged tissue; diseased tissue;

XX myeloid cell disorder; lymphoid cell disorder;

XX bone cartilage tissue growth; tendon tissue growth;

XX ligament tissue growth; nerve tissue growth; regeneration; wound healing;

XX tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.

XX Homo sapiens.

XX WO2003025148-A2.

XX 27-MAR-2003.

XX 19-SEP-2002; 2002WO-US029964.

XX 19-SEP-2001; 2001US-0323739P.

XX 13-SEP-2002; 2002US-00323739.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Auendi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

XX Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;

XX Haley-Vicente D;

XX WPI; 2003-354603/33.

XX N-PSDB; ADI21333.

XX New polynucleotides and secreted proteins, useful for treating myeloid or
 PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve
 PT tissue growth or regeneration, in wound healing, and in tissue repair and
 PT replacement.

XX Example 3; SEQ ID NO 804; 156pp; English.

XX The invention relates to an isolated polynucleotide encoding a
 CC polypeptide with biological activity. The polynucleotides and
 CC polypeptides are useful in diagnostics, forensics, gene mapping,
 CC identification of mutations responsible for genetic disorders and other
 CC traits, to assess biodiversity, as nutritional sources or supplements.
 CC The polynucleotides may also be used as molecular weight markers,
 CC chromosome markers or map related gene positions, or as an antigen to
 CC raise anti-DNA antibodies or elicit immune response. The polypeptides are
 CC useful for raising antibodies, as markers for tissues in which the
 CC corresponding polypeptide is expressed, for re-engineering damaged or
 CC diseased tissues, for treating myeloid or lymphoid cell disorders, in
 CC bone cartilage, tendon, ligament and/or nerve tissue growth or
 CC regeneration, in wound healing, in tissue repair and replacement, in
 CC healing of burns, incisions and ulcers, and in treating cancer. The
 CC present sequence represents the amino acid sequence of a novel human
 CC polypeptide.

XX
 SQ

Sequence 527 AA;

Query Match 100.0%; Score 2691; DB 7; Length 527;

Best Local Similarity 100.0%; Pred. No. 3.5e-249;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGELMLLVLAAREALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPD 60

Db 28 MRGELMLLVLAAREALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPD 87

QY 61 TQLSQDLGGGTGLAMDITLPDNRTRVVEDNHSYVYVSRSLYGPSEPHSRELWVDVAENRSQVK 120

Db 88 TQLSQDLGGGTGLAMDITLPDNRTRVVEDNHSYVYVSRSLYGPSEPHSRELWVDVAENRSQVK 147

QY 121 IHTILSNTHRQASRVLSFDPFPYGHPLRQITTIATGTFIPMGDVIHRMLTATQVAPLMA 180

Db 148 IHTILSNTHRQASRVLSFDPFPYGHPLRQITTIATGTFIPMGDVIHRMLTATQVAPLMA 207

QY 181 NFNPGYSNDSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOALHHDGRIVFAYKEIPM 240

Db 208 NFNPGYSNDSTVYFDNGTVFVQWDHVLQGWEDKGSFTFOALHHDGRIVFAYKEIPM 267

QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKVTSMASVFT 300

Db 268 SVPEISSQHPVKTGLSDAFMILNPSDPVPESSRRRSIFEYHRIELDPKVTSMASVFT 327

QY 301 LPTCLQHRSCDACMSDLTFNCWCHVLRQCSSGFDRYQEWMDYGCQAABGRMCBDFQ 360

Db 328 LPTCLQHRSCDACMSDLTFNCWCHVLRQCSSGFDRYQEWMDYGCQAABGRMCBDFQ 387

QY 361 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 420

Db 388 DEDHDSASPDTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPAGGGLQNNLSPKTKGT 447

QY 421 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 480

Db 448 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHST 507

QY 481 YAEVPSGHEKEGFMEAEQC 500

Db 508 YAEVPSGHEKEGFMEAEQC 527

RESULT 7

ABB90723

ID ABB90723 standard; protein; 1002 AA.

XX AC ABB90723;

XX 30-MAY-2002 (first entry)

XX Human Tumour Endothelial Marker polypeptide SEQ ID NO 179.

XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
 KW psoriasis.

XX Homo sapiens.

XX WO200210217-A2.

XX 07-FEB-2002.

XX 01-AUG-2001; 2001WO-US024031.

XX 02-AUG-2000; 2000US-0222599P.

XX 11-AUG-2000; 2000US-0224360P.

XX 11-APR-2001; 2001US-0282850P.

XX (UWJO) UNIV JOHNS HOPKINS.

XX St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2002-291856/33.
XX
XX An isolated molecule comprising an antibody variable region which
XX specifically binds to an extracellular domain of a tumor endothelial
XX marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Disclosure; Page 125-128; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
XX variable region which specifically binds to an extracellular domain of a
XX tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,
XX ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
XX proteins have cytostatic, immunostimulant and antiangiogenic activity.
XX They are useful for inhibiting tumor growth, neoangiogenesis in subjects
XX bearing a vascularised tumour, polycystic kidney disease, diabetic
XX retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
XX genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
XX are disclosed, as are marker oligonucleotide sequences: tumour
XX endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
XX endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
XX (PEM) ABL91903-ABL91995
XX
XX Sequence 1002 AA;
XX
XX Query Match 100.0%; Score 2691; DB 5; Length 1002;
XX Best Local Similarity 100.0%; Pred. No. 9.5e-249;
XX Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRGELWLLVLRRAALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSPDR 60
Db 503 MRGELWLLVLRRAALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSPDR 562
Qy 61 TQLSQDLGGGTGLAMDTLPDNRTRVEDNHSYVYVSRLYGPPSPHRELWVDVAEANRSQVK 120
Db 563 TQLSQDLGGGTGLAMDTLPDNRTRVEDNHSYVYVSRLYGPPSPHRELWVDVAEANRSQVK 622
Qy 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMA 180
Db 623 IHTILSNTHRQASRVLSFDPPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMA 682
Qy 181 NFNPYSDNSTVYFDNGTVFVQWDHVVYVQWEDKGSFTFOALHHDGRIVFAYKEIPM 240
Db 683 NFNPYSDNSTVYFDNGTVFVQWDHVVYVQWEDKGSFTFOALHHDGRIVFAYKEIPM 742
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300
Db 743 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 802
Qy 301 LPTCLOHRSQDCAKSSDLTFNCSCWCHVLQRCSSGFDRIYRQEMDYGCAQAEGRMCBDFQ 360
Db 803 LPTCLOHRSQDCAKSSDLTFNCSCWCHVLQRCSSGFDRIYRQEMDYGCAQAEGRMCBDFQ 862
Qy 361 DEHDSASPTSFSPYDGLTTTSSSIFDLSLTEDDTKLNYPAGGDLQNNLSPKTKGT 420
Db 863 DEHDSASPTSFSPYDGLTTTSSSIFDLSLTEDDTKLNYPAGGDLQNNLSPKTKGT 922
Qy 421 PVHLGTVIGIVLAVLLVAIIAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDHST 480
Db 923 PVHLGTVIGIVLAVLLVAIIAGIYINGHTPSNAALFFIERRPHHPAMKFRSHPDHST 982
Qy 481 YAEVPSGHEKEGFEAEQC 500
Db 983 YAEVPSGHEKEGFEAEQC 1002
XX
XX RESULT 8
XX ABUS4430
XX ID ABUS4430 standard; protein; 1002 AA.
XX
XX AC ABUS4430;

XX 12-MAR-2003 (first entry)
XX Human tumour endothelial marker TEM 8.
XX
XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
XX Tumour endothelial marker; normal endothelial marker; PEM;
XX pan-endothelial marker; polycystic kidney disease; psoriasis;
XX diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
XX neoangiogenesis; immune response; cytostatic; antidiabetic;
XX ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
XX
XX Homo sapiens.
XX WO200283874-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US008253.
XX
XX 11-APR-2001; 2001US-0282850P.
XX 06-FEB-2002; 2002US-0354262P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX
XX WPI; 2003-093016/08.
XX N-PSDB; ABX72003.
XX
XX New purified human transmembrane protein, designated as tumor endothelial
XX marker (TEM) 3, useful for detecting, diagnosing or treating tumours, or
XX polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
XX psoriasis.
XX
XX Disclosure; Page 122-124; 374pp; English.
XX
XX The present invention relates to a novel method for the isolation of
XX endothelial cells (ECs), and the identification of genes expressed in
XX normal and tumour ECs. Tumour endothelial marker (TEM), normal
XX endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
XX identified in human ECs. The human EC marker proteins and the
XX polynucleotide sequences encoding them are useful for detecting,
XX diagnosing or treating tumours as well as polycystic kidney disease,
XX diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
XX useful for inhibiting neoangiogenesis or tumour angiogenesis, for
XX inducing an immune response to tumour endothelial cells in a patient,
XX for identifying candidate drugs for treating tumours. The present
XX sequence represents a human TEM or NEM protein of the invention
XX
XX Sequence 1002 AA;
XX
XX Query Match 100.0%; Score 2691; DB 6; Length 1002;
XX Best Local Similarity 100.0%; Pred. No. 9.5e-249;
XX Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRGELWLLVLRRAALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSPDR 60
Db 503 MRGELWLLVLRRAALSPQAGHDEGPGSGWAAKGTVRGNRRARSPGHVSPDR 562
Qy 61 TQLSQDLGGGTGLAMDTLPDNRTRVEDNHSYVYVSRLYGPPSPHRELWVDVAEANRSQVK 120
Db 563 TQLSQDLGGGTGLAMDTLPDNRTRVEDNHSYVYVSRLYGPPSPHRELWVDVAEANRSQVK 622
Qy 121 IHTILSNTHRQASRVLSFDPPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMA 180
Db 623 IHTILSNTHRQASRVLSFDPPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLMA 682
Qy 181 NFNPYSDNSTVYFDNGTVFVQWDHVVYVQWEDKGSFTFOALHHDGRIVFAYKEIPM 240
Db 683 NFNPYSDNSTVYFDNGTVFVQWDHVVYVQWEDKGSFTFOALHHDGRIVFAYKEIPM 742
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTMSAVEFTP 300

Db 743 SVPEISSQHPVKTGLSDAFMILNPSDPVESRRSIFVYHRIELDFSKVTSMAVEFTP 802
Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLCRCSSGFDYRQEWMDYGCQAEGRMCDPQ 360
Db 803 LPTCLQHRSCDACMSSDLTFNCSCWCHVLCRCSSGFDYRQEWMDYGCQAEGRMCDPQ 862
Qy 361 DEHDSASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420
Db 863 DEHDSASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 922
Qy 421 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPANKFRSHPDHST 480
Db 923 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPANKFRSHPDHST 982
Qy 481 YAEVEPSGHEKEGFMEAEQC 500
Db 983 YAEVEPSGHEKEGFMEAEQC 1002

RESULT 9

AD121064
ID AD121064 standard; protein; 488 AA.

XX AC AD121064;

XX 15-APR-2004 (first entry)

XX Novel human protein #39.

XX forensic; nutritional source; damaged tissue; diseased tissue;

KW myeloid cell disorder; lymphoid cell disorder;

KW bone cartilage tissue growth; tendon tissue growth;

KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;

KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.

XX Homo sapiens.

XX W02003025148-A2.

XX 27-MAR-2003.

XX 19-SEP-2002; 2002WO-US029964.

XX 19-SEP-2001; 2001US-0323739P.

XX 13-SEP-2002; 2002US-00323739.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;

PI Haley-Vicente D;

XX WPI; 2003-354603/33.

XX N-PSDB; ADI21780.

XX New polynucleotides and secreted proteins, useful for treating myeloid or

PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve

PT tissue growth or regeneration, in wound healing, and in tissue repair and

PT replacement.

XX Claim 20; SEQ ID NO 315; 156pp; English.

XX The invention relates to an isolated polynucleotide encoding a

CC polypeptide with biological activity. The polynucleotides and

CC polypeptides are useful in diagnostics, forensics, gene mapping,

CC identification of mutations responsible for genetic disorders and other

CC traits, to assess biodiversity, as nutritional sources or supplements.

CC The polynucleotides may also be used as molecular weight markers,

CC chromosome markers or map related gene positions, or as an antigen to

CC raise anti-DNA antibodies or elicit immune response. The polypeptides are

CC useful for raising antibodies, as markers for tissues in which the

CC corresponding polypeptide is expressed, for re-engineering damaged or

CC diseased tissues, for treating myeloid or lymphoid cell disorders, in
CC bone cartilage, tendon, ligament and/or nerve tissue growth or
CC regeneration, in wound healing, in tissue repair and replacement, in
CC healing of burns, incisions and ulcers, and in treating cancer. The
CC present sequence represents the amino acid sequence of a novel human
CC protein.

XX SQ Sequence 488 AA;

Query Match 96.9%; Score 2607; DB 7; Length 488;

Best Local Similarity 97.6%; Pred. No. 3.7e-241;

Matches 488; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

Qy 1 MRGELWLLVLRRAALSPQAGHDEGPGSGAAKGTGVRNRRARSPGHVSPDR 60

Db 1 MRGELWLLVLRRAALSPQAGHDEGPGSGAAKGTGVRNRRARSPGHVSPDR 60

Qy 61 TQLSQDLGGGTGLAMDTLPNRTVRVEDNHSYVSRLYGPSEPHSRELWVDVAENRQVK 120

Db 61 TQLSQDLGGGTGLAMDTLPNRTVRVEDNHSYVSRLYGPSEPHSRELWVDVAENRQVK 120

Qy 121 IHTILSNTHRQASRVLSDFPFYGHPLRQITATGGFIFMGDVVHRMLTATQYVAPLMA 180

Db 121 IHTILSNTHRQASRVLSDFPFYGHPLRQITATGGFIFMGDVVHRMLTATQYVAPLMA 180

Qy 181 NFNPYSDNSTVYVFDNGTVVQWDHVYVQWDEKGSFTFOALHHDGRIVFAYKEIPM 240

Db 181 NFNPYSDNSTVYVFDNGTVVQWDHVYVQWDEKGSFTFOALHHDGRIVFAYKEIPM 240

Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVESRRSIFVYHRIELDFSKVTSMAVEFTP 300

Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVESRRSIFVYHRIELDFSKVTSMAVEFTP 300

Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLCRCSSGFDYRQEWMDYGCQAEGRMCDPQ 360

Db 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLCRCSSGFDYRQEWMDYGCQAEGRMCDPQ 360

Qy 361 DEHDSASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 420

Db 361 DEHDSASPTSFSPYDGLTTSSSLFIDSLTTEDDTKLNYPAGGDLQNNLSPKTKGT 408

Qy 421 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPANKFRSHPDHST 480

Db 409 PVHLGTVIGIVLAVLLVAAILAGIYINGHPTSNAAFFIERRPHHPANKFRSHPDHST 468

Qy 481 YAEVEPSGHEKEGFMEAEQC 500

Db 469 YAEVEPSGHEKEGFMEAEQC 488

RESULT 10

ABB90783

ID ABB90783 standard; protein; 500 AA.

XX AC ABB90783;

XX 30-MAY-2002 (first entry)

Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 297.

Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
normal endothelial marker; pan-endothelial marker; immunostimulant;
antiangiogenic; tumour; neovascularisation; vascularised tumour;
polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
psoriasis.

XX Mus musculus.

XX W0200210217-A2.

XX 07-FEB-2002.

XX 01-AUG-2001; 2001WO-US024031.

XX PR 02-AUG-2000; 2000US-0222599P.
 XX PR 11-AUG-2000; 2000US-0224360P.
 XX PR 11-APR-2001; 2001US-0282850P.
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX St Croix B, Kinzler KW, Vogelstein B;
 DR WPI; 2002-291856/33.
 DR N-PSDB; ABL92136.
 XX
 PT An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
 XX Disclosure; Page 301-302; 331pp; English.
 XX The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90740, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and angiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (PEM) ABL91903-ABL91995

Query Match 82.1%; Score 2209; DB 5; Length 500;
 Best Local Similarity 81.6%; Pred. No. 7e-203;
 Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;

QY	1	MRCGLMLL-VLVLEAARALSPQAGHDGPGSGAAKGTVRGWNRARRSPGHVSEPD	59
DB	1	MRAQLMQLQLLLRGAARALSPTATPAGNEGODSATAKTQTQGSRRPRESPAQVLKPG	60
QY	60	RTQLSDQLGGTTLAMDTPDNRTRVVEDNHYSYVRLYGPSPHRELWVDVAENRSOV	119
DB	61	KTIILSSSHROASRVLSDFPFYGHPLRQITATGGFIKMGDLHRLMTATQVAPLM	120
QY	120	KIHTILSNTHROASRVLSDFPFYGHPLRQITATGGFIKMGDLHRLMTATQVAPLM	179
DB	121	KIHLISSSHROASRVLSDFPFYGHPLRQITATGGFIKMGDLHRLMTATQVAPLM	180
QY	180	ANFNPYGSDNSTVVFYVQMDHVYLQGWEDKGSFTFQAALHHDGRIVFYKBP	239
DB	181	ANFNPYGSDNSTVAYFDNGTVFVQWDHYVLQDREDGTSFTFQAALHRDRGVFGYKEIP	240
QY	240	MSVPETISSQHPPVKTGSLDAFMILNDPDPVPSRRSRSTFEYHRIELDSPKVTSMASVEFT	299
DB	241	MAVLDISSAQHPYKAGSLDAFMILNSSPVSQRRTTFEYHRELDSSKITTTSAVEFT	300
QY	300	PLPTCLQHRSCDACMSDLTFNCWCWCHVLQRCSSGFDRYRQSWMDYGCQAERGMCDF	359
DB	301	PLPTCLQHQCDTCVSNLTIFNCWCWCHVLQRCSSGFDRYRQWBLYGCAQBAEGKTCDF	360
QY	360	QDEHDHASGPDTSFSPYDGDLTTTSSSLFIDSLTTDDTKLNPNYAGGDLQNLSPKTKG	419
DB	361	QDDSHYSAGSDSFSPENG-D-STTSSSLFIDSLTTDDTKLPNYAEGDGLPDHSPSKSG	419
QY	420	TPVHLGTIGVILAVLLVAAILLAGIYINGHPTSNAAALFFIERPHHWPMKFRSHPDHS	479
DB	420	PPVHLGTIGVILAVLLVAAILLAGIYISGHFNPSNAALFFIERPHHWPMKFRHNPHNS	479
QY	480	TYAEVFPSGHEKGFMEABQC	500
DB	480	TYTEVFPSGHEKGFVEAOC	500

RESULT 11
 ABB90729
 ID ABB90729 standard; protein; 500 AA.
 XX AC ABB90729;
 XX DT 30-MAY-2002 (first entry)
 XX DE Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 192.
 XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psoriasis.
 XX OS Mus musculus.
 XX PN WO200210217-A2.
 XX PD 07-FEB-2002.
 XX PF 01-AUG-2001; 2001WO-US024031.
 XX PR 02-AUG-2000; 2000US-0222599P.
 PR 11-AUG-2000; 2000US-0224360P.
 PR 11-APR-2001; 2001US-0282850P.
 XX PA (UYJO) UNIV JOHNS HOPKINS.
 XX St Croix B, Kinzler KW, Vogelstein B;
 DR WPI; 2002-291856/33.
 XX An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
 PS Disclosure; Page 146-147; 331pp; English.

Query Match 82.1%; Score 2209; DB 5; Length 500;
 Best Local Similarity 81.6%; Pred. No. 7e-203;
 Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;

QY	1	MRCGLMLL-VLVLEAARALSPQAGHDGPGSGAAKGTVRGWNRARRSPGHVSEPD	59
DB	1	MRAQLMQLQLLLRGAARALSPTATPAGNEGODSATAKTQTQGSRRPRESPAQVLKPG	60
QY	60	RTQLSDQLGGTTLAMDTPDNRTRVVEDNHYSYVRLYGPSPHRELWVDVAENRSOV	119
DB	61	KTIILSSSHROASRVLSDFPFYGHPLRQITATGGFIKMGDLHRLMTATQVAPLM	120
QY	120	KIHTILSNTHROASRVLSDFPFYGHPLRQITATGGFIKMGDLHRLMTATQVAPLM	179
DB	121	KIHLISSSHROASRVLSDFPFYGHPLRQITATGGFIKMGDLHRLMTATQVAPLM	180
QY	180	ANFNPYGSDNSTVVFYVQMDHVYLQGWEDKGSFTFQAALHHDGRIVFYKBP	239
DB	181	ANFNPYGSDNSTVAYFDNGTVFVQWDHYVLQDREDGTSFTFQAALHRDRGVFGYKEIP	240
QY	240	MSVPETISSQHPPVKTGSLDAFMILNDPDPVPSRRSRSTFEYHRIELDSPKVTSMASVEFT	299
DB	241	MAVLDISSAQHPYKAGSLDAFMILNSSPVSQRRTTFEYHRELDSSKITTTSAVEFT	300
QY	300	PLPTCLQHRSCDACMSDLTFNCWCWCHVLQRCSSGFDRYRQSWMDYGCQAERGMCDF	359
DB	301	PLPTCLQHQCDTCVSNLTIFNCWCWCHVLQRCSSGFDRYRQWBLYGCAQBAEGKTCDF	360
QY	360	QDEHDHASGPDTSFSPYDGDLTTTSSSLFIDSLTTDDTKLNPNYAGGDLQNLSPKTKG	419
DB	361	QDDSHYSAGSDSFSPENG-D-STTSSSLFIDSLTTDDTKLPNYAEGDGLPDHSPSKSG	419
QY	420	TPVHLGTIGVILAVLLVAAILLAGIYINGHPTSNAAALFFIERPHHWPMKFRSHPDHS	479
DB	420	PPVHLGTIGVILAVLLVAAILLAGIYISGHFNPSNAALFFIERPHHWPMKFRHNPHNS	479
QY	480	TYAEVFPSGHEKGFMEABQC	500
DB	480	TYTEVFPSGHEKGFVEAOC	500

Db 121 VVFDNGTVFVQWHDVYVLOGWEDKGSFTFQALHHDGRIVFAYKEIPMSVPEISSQHP 180
 Qy 252 VKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTPLTCLQHRSCD 311
 Db 181 VKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTPLTCLQHRSCD 240
 Qy 312 ACMSSDLTFNCSWCHVLQRCSSGDFRYRQEW-MDYGCAQAEAGRMCDQD-----ED 363
 Db 241 ACMSSDLTFNCSWCHVLQRCSSGDFRYRQEW-MDYGCAQAEAGRMCDQD-----QDVRGLPGMRT 294
 Qy 364 HDSASPDTSFSPYDGLTFTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPTKGTGPVH 423
 Db 295 TTSASPDTSFSPYDGLTFTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPTKGTGPVH 354
 Qy 424 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHDPHSTYAE 483
 Db 355 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHDPHSTYAE 414
 Qy 484 VEPGHEKEGFMFAEQC 500
 Db 415 VEPGHEKEGFMFAEQC 431

RESULT 15

AB001434
 ID AB001434 standard; protein; 431 AA.

AC AB001434;

DT 07-AUG-2003 (first entry)

XX Human tumour endothelial marker 7 precursor protein.

XX Human; gene therapy; stem cell inducer; osteoporosis; regeneration;
 XX stem cell growth factor-like activity; leukaemia; haemophilia; allergy;
 XX Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis;
 XX autoimmune disease; multiple sclerosis; systemic lupus erythematosus;
 XX graft-versus-host disease; degenerative disease; Alzheimer's disease;
 XX osteoarthritis; anaemia; tendonitis; carpal tunnel syndrome; cancer;
 XX tumour endothelial marker 7 precursor.

XX Homo sapiens.

XX US2003022825-A1.

XX 30-JAN-2003.

PF 24-JUL-2001; 2001US-00912935.

PR 23-DEC-2000; 2000WO-US035260.

XX (NISH/) NISHIKAWA M.

PA (LABA/) LABAT I.

PA (DRMA/) DRMANAC R T.

PA (TANG/) TANG Y T.

PA (CHAO/) CHAO C.

XX Nishikawa M, Labat I, Drmanac RT, Tang YT, Chao C;

XX WPI; 2003-456302/43.

XX New stem cell growth factor-like polypeptides and polynucleotides, useful
 XX for treating e.g. leukemia, hemophilia, osteoporosis, osteoarthritis,
 XX graft-versus-host disease, cancers, Alzheimer's disease, Huntington's
 XX disease.

XX Example 4; Fig 2; 98pp; English.

XX PS

XX XX

XX The invention relates to a new isolated polypeptide, which has stem cell
 XX growth factor-like activity. The new polypeptide, the polynucleotide
 XX encoding this polypeptide, or the agonist of the polypeptide are useful
 XX for treating a subject in need of enhanced activity or expression of stem
 XX cell growth factor-like polypeptide. The antagonist of the polypeptide or

CC the polynucleotide is useful for treating a subject in need to inhibit
 CC the activity or expression of stem cell growth factor-like polypeptide.
 CC The new polypeptide or polynucleotide is particularly useful for inducing
 CC differentiation of embryonic and adult stem cells to give rise to
 CC different cell types. In particular, the polypeptide or polynucleotide is
 CC useful for treating leukaemia, haemophilia, osteoporosis, osteoarthritis,
 CC anaemia, tendonitis, carpal tunnel syndrome, autoimmune diseases (e.g.
 CC multiple sclerosis, systemic lupus erythematosus, graft-versus-host
 CC disease or allergies), cancers or degenerative diseases (e.g. Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease or amyotrophic lateral
 CC sclerosis) or for generating new tissues and organs that may aid patients
 CC in need of transplanted tissues. The polynucleotide may also be used in
 CC gene therapy for the treatment of these diseases. The new polypeptide or
 CC polynucleotide is also useful in diagnostic or research methods. The
 CC present sequence represents the human tumour endothelial marker 7
 CC precursor protein

XX SQ Sequence 431 AA;

Query Match 81.2%; Score 2185; DB 6; Length 431;

Best Local Similarity 95.2%; Pred. No. 1.1e-200;

Matches 416; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

Qy 72 LAMDTLPDNRTRVVDNHSYVSRLYGSPSPHRELWVDVAENRSQVKIHTILSNTHRQ 131

Db 1 LAMDTLPDNRTRVVDNHSYVSRLYGSPSPHRELWVDVAENRSQVKIHTILSNTHRQ 60

Qy 132 ASRVLSDFPFFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPYSONST 191

Db 61 ASRVLSDFPFFYGHPLRQITATGGFIFMGDVIHRMLTATQYVAPLMANFNPYSONST 120

Qy 192 VVFDNGTVFVQWHDVYVLOGWEDKGSFTFQALHHDGRIVFAYKEIPMSVPEISSQHP 251

Db 121 VVFDNGTVFVQWHDVYVLOGWEDKGSFTFQALHHDGRIVFAYKEIPMSVPEISSQHP 180

Qy 252 VKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTPLTCLQHRSCD 311

Db 181 VKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVEFTPLTCLQHRSCD 240

Qy 312 ACMSSDLTFNCSWCHVLQRCSSGDFRYRQEW-MDYGCAQAEAGRMCDQD-----ED 363

Db 241 ACMSSDLTFNCSWCHVLQRCSSGDFRYRQEW-MDYGCAQAEAGRMCDQD-----QDVRGLPGMRT 294

Qy 364 HDSASPDTSFSPYDGLTFTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPTKGTGPVH 423

Db 295 TTSASPDTSFSPYDGLTFTSSSLFIDSLTDDTKLNPYAGDGLQNNLSPTKGTGPVH 354

Qy 424 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHDPHSTYAE 483

Db 355 LGTIVGIVLAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHDPHSTYAE 414

Qy 484 VEPGHEKEGFMFAEQC 500

Db 415 VEPGHEKEGFMFAEQC 431

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OM protein - protein search, using sw model

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Title: US-09-918-715-230

Perfect score: 2691

Sequence: 1 MRGELMLLVLRRAARALS.....YAEVPSGHEKEGFMEAEQC 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Maximum Match 100%

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Database :

Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2691	100.0	500	10	US-09-918-715-230
2	2691	100.0	500	15	US-10-435-696-79
3	2691	100.0	500	16	US-10-474-794-230
4	2691	100.0	500	16	US-10-357-819-2
5	2691	100.0	500	18	US-10-979-159-230
6	2691	100.0	1002	10	US-09-918-715-179
7	2691	100.0	1002	16	US-10-474-794-179
8	2691	100.0	1002	18	US-10-979-159-179
9	2602	96.7	488	16	US-10-357-819-4
10	2566	95.4	502	14	US-10-156-487A-5
11	2209	82.1	500	10	US-09-918-715-192

12	2209	82.1	500	10	US-09-918-715-297	Sequence 297, App
13	2209	82.1	500	14	US-10-156-487A-6	Sequence 6, Appli
14	2209	82.1	500	16	US-10-474-794-192	Sequence 192, App
15	2209	82.1	500	16	US-10-474-794-297	Sequence 297, App
16	2209	82.1	500	18	US-10-979-159-192	Sequence 192, App
17	2209	82.1	500	18	US-10-979-159-297	Sequence 297, App
18	2185	81.2	431	10	US-09-912-935-36	Sequence 36, Appl
19	2185	81.2	431	15	US-10-168-365-36	Sequence 36, Appl
20	1295	48.1	499	10	US-09-912-935-31	Sequence 31, Appl
21	1295	48.1	499	15	US-10-168-365-31	Sequence 31, Appl
22	1295	48.1	529	10	US-09-918-715-189	Sequence 189, App
23	1295	48.1	529	10	US-09-918-715-200	Sequence 200, App
24	1295	48.1	529	10	US-09-912-935-28	Sequence 28, Appl
25	1295	48.1	529	10	US-09-912-935-40	Sequence 40, Appl
26	1295	48.1	529	14	US-10-156-487A-4	Sequence 4, Appli
27	1295	48.1	529	15	US-10-168-365-28	Sequence 28, Appl
28	1295	48.1	529	16	US-10-474-794-189	Sequence 189, App
29	1295	48.1	529	16	US-10-474-794-200	Sequence 200, App
30	1295	48.1	529	18	US-10-979-159-189	Sequence 189, App
31	1295	48.1	529	18	US-10-979-159-200	Sequence 200, App
32	1294	48.1	529	13	US-10-052-586-472	Sequence 472, App
33	1294	48.1	529	13	US-10-066-500-128	Sequence 128, App
34	1294	48.1	529	14	US-10-174-590-472	Sequence 472, App
35	1294	48.1	529	14	US-10-176-758-472	Sequence 472, App
36	1294	48.1	529	14	US-10-175-737-472	Sequence 472, App
37	1294	48.1	529	14	US-10-174-581-472	Sequence 472, App
38	1294	48.1	529	14	US-10-176-483-472	Sequence 472, App
39	1294	48.1	529	14	US-10-176-749-472	Sequence 472, App
40	1294	48.1	529	14	US-10-176-914-472	Sequence 472, App
41	1294	48.1	529	14	US-10-176-915-472	Sequence 472, App
42	1294	48.1	529	14	US-10-173-706-472	Sequence 472, App
43	1294	48.1	529	14	US-10-175-738-472	Sequence 472, App
44	1294	48.1	529	14	US-10-175-752-472	Sequence 472, App
45	1294	48.1	529	14	US-10-176-482-472	Sequence 472, App

ALIGNMENTS

RESULT 1
US-09-918-715-230
; Sequence 230, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT FILING DATE: 2001-08-01
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-230

Query Match 100.0%; Score 2691; DB 10; Length 500;
Best Local Similarity 100.0%; Pred. No. 8.3e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELMLLVLRRAARALSPPQAGHDGPGSGWAAKGTIVGWNRRRARESPGHVSEPR 60
Db 1 MRGELMLLVLRRAARALSPPQAGHDGPGSGWAAKGTIVGWNRRRARESPGHVSEPR 60

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Qy 61 TOLSDQLGGGTAMDITLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
Db 61 TOLSDQLGGGTAMDITLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
Qy 121 IHTILSNTHRQASRVLSFDPPFGHPRLQRIITATGCFIFMGDDVIHRMLTATQVAPLMA 180
Db 121 IHTILSNTHRQASRVLSFDPPFGHPRLQRIITATGCFIFMGDDVIHRMLTATQVAPLMA 180
Qy 181 NFNPgySDNSTVYFDNGTVFVQWHDHVLQGWEDKGSFTFOALHHDGRIVPAYKEIPM 240
Db 181 NFNPgySDNSTVYFDNGTVFVQWHDHVLQGWEDKGSFTFOALHHDGRIVPAYKEIPM 240
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVFTTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVFTTP 300
Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSSGFDYRQEWMDYGCQAEGRMCDQ 360
Db 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSSGFDYRQEWMDYGCQAEGRMCDQ 360
Qy 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
Db 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
Qy 421 PVHLGTTIGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTTIGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 481 YAEVPSGHEKEGFMEAEQC 500

RESULT 2
US-10-435-696-79
; Sequence 79, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
; APPLICANT: Witz, Ralph
; APPLICANT: Munnes, Marc
; APPLICANT: Kallabis, Harald
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
; FILE REFERENCE: Lea 36 108
; CURRENT APPLICATION NUMBER: US/10/435.696
; PRIOR FILING DATE: 2003-05-09
; CURRENT APPLICATION NUMBER: EP03003112.4
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 79
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-435-696-79

Query Match 100.0%; Score 2691; DB 15; Length 500;
Best Local Similarity 100.0%; Pred. No. 8.3e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLRRAAALSPOGAGHDEGPGSGWAAKGTVRGNRRARSPGHVSPDR 60
Db 1 MRGELWLLVLVLRRAAALSPOGAGHDEGPGSGWAAKGTVRGNRRARSPGHVSPDR 60
Qy 61 TOLSDQLGGGTAMDITLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
Db 61 TOLSDQLGGGTAMDITLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
Qy 121 IHTILSNTHRQASRVLSFDPPFGHPRLQRIITATGCFIFMGDDVIHRMLTATQVAPLMA 180
Db 121 IHTILSNTHRQASRVLSFDPPFGHPRLQRIITATGCFIFMGDDVIHRMLTATQVAPLMA 180
Qy 181 NFNPgySDNSTVYFDNGTVFVQWHDHVLQGWEDKGSFTFOALHHDGRIVPAYKEIPM 240
Db 181 NFNPgySDNSTVYFDNGTVFVQWHDHVLQGWEDKGSFTFOALHHDGRIVPAYKEIPM 240
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVFTTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVFTTP 300
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Qy 181 NFNPgySDNSTVYFDNGTVFVQWHDHVLQGWEDKGSFTFOALHHDGRIVPAYKEIPM 240
Db 181 NFNPgySDNSTVYFDNGTVFVQWHDHVLQGWEDKGSFTFOALHHDGRIVPAYKEIPM 240
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVFTTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVFTTP 300
Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSSGFDYRQEWMDYGCQAEGRMCDQ 360
Db 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSSGFDYRQEWMDYGCQAEGRMCDQ 360
Qy 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
Db 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
Qy 421 PVHLGTTIGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTTIGIVLAVLLVAAILLAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 481 YAEVPSGHEKEGFMEAEQC 500

RESULT 3
US-10-474-794-230
; Sequence 230, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474.794
; PRIOR FILING DATE: 2003-10-14
; CURRENT APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-230

Query Match 100.0%; Score 2691; DB 16; Length 500;
Best Local Similarity 100.0%; Pred. No. 8.3e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLRRAAALSPOGAGHDEGPGSGWAAKGTVRGNRRARSPGHVSPDR 60
Db 1 MRGELWLLVLVLRRAAALSPOGAGHDEGPGSGWAAKGTVRGNRRARSPGHVSPDR 60
Qy 61 TOLSDQLGGGTAMDITLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
Db 61 TOLSDQLGGGTAMDITLPDNRTRVVEDNHSYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
Qy 121 IHTILSNTHRQASRVLSFDPPFGHPRLQRIITATGCFIFMGDDVIHRMLTATQVAPLMA 180
Db 121 IHTILSNTHRQASRVLSFDPPFGHPRLQRIITATGCFIFMGDDVIHRMLTATQVAPLMA 180
Qy 181 NFNPgySDNSTVYFDNGTVFVQWHDHVLQGWEDKGSFTFOALHHDGRIVPAYKEIPM 240
Db 181 NFNPgySDNSTVYFDNGTVFVQWHDHVLQGWEDKGSFTFOALHHDGRIVPAYKEIPM 240
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVFTTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSVTSMASVFTTP 300
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Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDSPKVTSMASVEFTP 300
Qy 301 LPTCLOHRSQDACMSSDLTFCNSCHVLRQCSGFDYRQWMDYGCQAEGRMCEDFQ 360
Db 301 LPTCLOHRSQDACMSSDLTFCNSCHVLRQCSGFDYRQWMDYGCQAEGRMCEDFQ 360
Qy 361 DEHDSASPTSPSPYDGLTDTTSSSLFIDSLTDEDTKLNYPAGDGLQNNLSPKTKGT 420
Db 361 DEHDSASPTSPSPYDGLTDTTSSSLFIDSLTDEDTKLNYPAGDGLQNNLSPKTKGT 420
Qy 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHTPSNAALFFIERRPHHPAMPKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHTPSNAALFFIERRPHHPAMPKFRSHPDHST 480
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 481 YAEVPSGHEKEGFMEAEQC 500

RESULT 4
US-10-357-819-2
; Sequence 2, Application US/10357819
; Publication No. US20040259774A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Baha A.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Ji, Weizhen
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: Miller, Charles E.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-538A
; CURRENT APPLICATION NUMBER: US/10/357,819
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/584,411
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/783,436
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 10/085,198
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/353,301
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/355,099
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/356,424
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/358,239
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/358,608
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/359,367
; PRIOR FILING DATE: 2002-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 2
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-357-819-2
Query Match 100.0%; Score 2691; DB 16; Length 500;
Best Local Similarity 100.0%; Pred. No. 8.3e-249;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRGELMLLVLAAREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPDFR 60
Db 1 MRGELMLLVLAAREARALSPQAGHDEGPGSGAAKGTVRGNRRRARESPGHVSEPDFR 60
Qy 61 TQSQDLGGTGLAMDTLPNRTVRVEDNHSYVYRSLYGPSEPHSRRLVWVDAENRSQVK 120
Db 61 TQSQDLGGTGLAMDTLPNRTVRVEDNHSYVYRSLYGPSEPHSRRLVWVDAENRSQVK 120
Qy 121 IHTILSNTHRQASRVVLSDFPFVGHPLRQITATGCFIEMGDVHRLMLTATQYVAPLMA 180
Db 121 IHTILSNTHRQASRVVLSDFPFVGHPLRQITATGCFIEMGDVHRLMLTATQYVAPLMA 180
Qy 181 NFNPYSDNSTVYVYFQNGVTVVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Db 181 NFNPYSDNSTVYVYFQNGVTVVQWDHVLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM 240
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDSPKVTSMASVEFTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDSPKVTSMASVEFTP 300
Qy 301 LPTCLOHRSQDACMSSDLTFCNSCHVLRQCSGFDYRQWMDYGCQAEGRMCEDFQ 360
Db 301 LPTCLOHRSQDACMSSDLTFCNSCHVLRQCSGFDYRQWMDYGCQAEGRMCEDFQ 360
Qy 361 DEHDSASPTSPSPYDGLTDTTSSSLFIDSLTDEDTKLNYPAGDGLQNNLSPKTKGT 420
Db 361 DEHDSASPTSPSPYDGLTDTTSSSLFIDSLTDEDTKLNYPAGDGLQNNLSPKTKGT 420
Qy 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHTPSNAALFFIERRPHHPAMPKFRSHPDHST 480
Db 421 PVHLGTIVGIVLAVLLVAAILLAGIYINGHTPSNAALFFIERRPHHPAMPKFRSHPDHST 480
Qy 481 YAEVPSGHEKEGFMEAEQC 500
Db 481 YAEVPSGHEKEGFMEAEQC 500

RESULT 5
US-10-979-159-230
; Sequence 230, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 230
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-159-230
Query Match 100.0%; Score 2691; DB 18; Length 500;
Best Local Similarity 100.0%; Pred. No. 8.3e-249;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLRARALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPD 60
Db
Qy 1 MRGELWLLVLVLRARALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPD 60
Db
Qy 61 TQLSQDLGGGTAMDITLPDNRTRVVDNHSYYSRLYGPSPHSHRELWVDVAENRSQVK 120
Db 61 TQLSQDLGGGTAMDITLPDNRTRVVDNHSYYSRLYGPSPHSHRELWVDVAENRSQVK 120
Qy 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITTIATGGFIEMGDVIHRLMTATQVAPLMA 180
Db 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITTIATGGFIEMGDVIHRLMTATQVAPLMA 180
Qy 181 NFNPGYSDNSTVYFDNGTVFVQWHDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240
Db 181 NFNPGYSDNSTVYFDNGTVFVQWHDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDSPKVTSMASVEFTP 300
Db 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDSPKVTSMASVEFTP 300
Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCDPQ 360
Db 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCDPQ 360
Qy 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
Db 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
Qy 421 PVHLGTTIVGLVAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 421 PVHLGTTIVGLVAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Qy 481 YAEVEPSGHEKEGFMAEQ 500
Db 481 YAEVEPSGHEKEGFMAEQ 500

RESULT 6

US-09-918-715-179
; Sequence 179, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107 00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-179

Query Match 100.0%; Score 2691; DB 10; Length 1002;
Best Local Similarity 100.0%; Pred. No. 2.5e-248;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLRARALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPD 60
Db 503 MRGELWLLVLVLRARALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPD 562

Qy 61 TQLSQDLGGGTAMDITLPDNRTRVVDNHSYYSRLYGPSPHSHRELWVDVAENRSQVK 120
Db 563 TQLSQDLGGGTAMDITLPDNRTRVVDNHSYYSRLYGPSPHSHRELWVDVAENRSQVK 622
Qy 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITTIATGGFIEMGDVIHRLMTATQVAPLMA 180
Db 623 IHTILSNTHRQASRVLSFDFPFYGHPLRQITTIATGGFIEMGDVIHRLMTATQVAPLMA 682
Qy 181 NFNPGYSDNSTVYFDNGTVFVQWHDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240
Db 683 NFNPGYSDNSTVYFDNGTVFVQWHDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 742
Qy 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDSPKVTSMASVEFTP 300
Db 743 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDSPKVTSMASVEFTP 802
Qy 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCDPQ 360
Db 803 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDYRQEWMDYGCQAEGRMCDPQ 862
Qy 361 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 420
Db 863 DEDHDSASPTSFSPYDGLTTTSSSLFIDSLTTEDDTKLNYPYAGDGLQNNLSPKTKGT 922
Qy 421 PVHLGTTIVGLVAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 480
Db 923 PVHLGTTIVGLVAVLLVAAILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPDHST 982
Qy 481 YAEVEPSGHEKEGFMAEQ 500
Db 983 YAEVEPSGHEKEGFMAEQ 1002

RESULT 7

US-10-474-794-179
; Sequence 179, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-179

Query Match 100.0%; Score 2691; DB 16; Length 1002;
Best Local Similarity 100.0%; Pred. No. 2.5e-248;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGELWLLVLVLRARALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPD 60
Db 503 MRGELWLLVLVLRARALSPQAGHDEGPGSGAAKGTVRGWNRRARSPGHVSEPD 562
Qy 61 TQLSQDLGGGTAMDITLPDNRTRVVDNHSYYSRLYGPSPHSHRELWVDVAENRSQVK 120
Db 563 TQLSQDLGGGTAMDITLPDNRTRVVDNHSYYSRLYGPSPHSHRELWVDVAENRSQVK 622
Qy 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITTIATGGFIEMGDVIHRLMTATQVAPLMA 180
Db 623 IHTILSNTHRQASRVLSFDFPFYGHPLRQITTIATGGFIEMGDVIHRLMTATQVAPLMA 682


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; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-357-819-4

Query Match      96.7%; Score 2602; DB 16; Length 488;
Best Local Similarity 97.4%; Pred. No. 2.8e-240;
Matches 487; Conservative 1; Mismatches 0; Indels 12; Gaps 1;

QY 1 MRGELWLLVLVLRRAAALSPQAGHDEGPGSGAAKGTVRGWNRRARESFGHVSFDR 60
DQ 1 MRGELWLLVLVLRRAAALSPQAGHDEGPGSGAAKGTVRGWNRRARESFGHVSFDR 60
DB 1 MRGELWLLVLVLRRAAALSPQAGHDEGPGSGAAKGTVRGWNRRARESFGHVSFDR 60
QY 61 TQSLQDLGGGTAMDTLPDNRTRVVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120
DQ 61 TQSLQDLGGGTAMDTLPDNRTRVVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120
DB 61 TQSLQDLGGGTAMDTLPDNRTRVVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120
QY 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITATGGFIIMGDVIIHRMLTATQYVAPLMA 180
DQ 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITATGGFIIMGDVIIHRMLTATQYVAPLMA 180
DB 121 IHTILSNTHRQASRVLSFDFPFYGHPLRQITATGGFIIMGDVIIHRMLTATQYVAPLMA 180
QY 181 NFNPYSDNSTVYFVQWHDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240
DQ 181 NFNPYSDNSTVYFVQWHDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240
DB 181 NFNPYSDNSTVYFVQWHDHVLQGWEDKGSFTFOAALHHDGRIVPAYKEIPM 240
QY 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDSPSKVTSMAVEFTP 300
DQ 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDSPSKVTSMAVEFTP 300
DB 241 SVPEISSQHPVKTGLSDAFMILNPSDPVPSRRRSIFEYHRIELDSPSKVTSMAVEFTP 300
QY 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDYRQEWMDYCAQAEGRMCEDFQ 360
DQ 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDYRQEWMDYCAQAEGRMCEDFQ 360
DB 301 LPTCLQHRSCDACMSSDLTFNCSCWCHVLRQCSGFDYRQEWMDYCAQAEGRMCEDFQ 360
QY 361 DEHDASPDTSFSPYDGLTTSSTSSLFIDSITTTEDDTKLNYPAGDGLQNNLSPKTKGT 420
DQ 361 DEHDASPDTSFSPYDGLTTSSTSSLFIDSITTTEDDTKLNYPAGDGLQNNLSPKTKGT 420
DB 361 DEHDASPDTSFSPYDGLTTSSTSSLFIDSITTTEDDTKLNYPAGDGLQNNLSPKTKGT 420
QY 421 PVHLGTTIGVILVLAIVAAIILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPHST 480
DQ 421 PVHLGTTIGVILVLAIVAAIILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPHST 480
DB 421 PVHLGTTIGVILVLAIVAAIILAGIYINGHPTSNAAALFFIERRPHHPAMKFRSHPHST 480
QY 481 YAEVPSGHEKEGFMFAEQC 500
DQ 481 YAEVPSGHEKEGFMFAEQC 500
DB 481 YAEVPSGHEKEGFMFAEQC 500

RESULT 10
US-10-156-487A-5
; Sequence 5, Application US/10156487A
; Publication No. US20030092025A1
; GENERAL INFORMATION:
; APPLICANT: Juan, Todd
; APPLICANT: Bass, Michael B.
; APPLICANT: Oliner, John
; TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
; FILE REFERENCE: 01-072-A
; CURRENT APPLICATION NUMBER: US/10/156,487A
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/293,852
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-156-487A-5

Query Match      95.4%; Score 2566; DB 14; Length 502;
Best Local Similarity 95.9%; Pred. No. 8.3e-237;
Matches 487; Conservative 0; Mismatches 7; Indels 14; Gaps 3;

QY 1 MRGELWLLVLVLRRAAALSPQAGHDEGPGSGAAKGTVRGWNRRARESFGHVSFDR 60
DQ 1 MRGELWLLVLVLRRAAALSPQAGHDEGPGSGAAKGTVRGWNRRARESFGHVSFDR 60
DB 1 MRGELWLLVLVLRRAAALSPQAGHDEGPGSGAAKGTVRGWNRRARESFGHVSFDR 60
QY 60 RTQSLQDLGGGTAMDTLPDNRTRVVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 119
DQ 60 RTQSLQDLGGGTAMDTLPDNRTRVVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 119
DB 60 RTQSLQDLGGGTAMDTLPDNRTRVVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 119
QY 61 KTQSLQDLGGGTAMDTLPDNRTRVVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120
DQ 61 KTQSLQDLGGGTAMDTLPDNRTRVVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120
DB 61 KTQSLQDLGGGTAMDTLPDNRTRVVEDNHSYYSRLYGPSEPHSRELWVDVAEANSQVK 120
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Qy 360 QDEHDSASDPTSPSPVDGDLTTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPTKKG 419
Db 361 QDDSHYASDPSSFPNGD-STTSSSLFIDSLTTEDDTKLNYPAGDGLPDHSSPKSKG 419
Qy 420 TPVHLGTIVGVLAVLVAAILAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHS 479
Db 420 PPVHLGTIVGVLAVLVAAILAGIYISGHPNSNAALFFIERRPHWPAMKFRSHPDHS 479
Qy 480 TYAEVPSGHEKEGFVEAEQC 500
Db 480 TYTEVEPSGHEKEGFVEAEQC 500

RESULT 14
US-10-474-794-192
; Sequence 192, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-474-794-192

Query Match 82.1%; Score 2209; DB 16; Length 500;
Best Local Similarity 81.6%; Pred. No. 1.5e-202;
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MRGELWLL-VLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRARSPGHVSEPD 59
Db 1 MRAQLWLLQLLLRGAARALSPATPAGHNEGQDSAWTAKTRQGSRRPRESPAQVLKPG 60
Qy 60 RTQLSQDLGGGTLAMDTPDNRTRVVDNHSYYVSRLYGPSEPHSRELWVDVAEANSQV 119
Db 61 KTQLSQDLGGGSLAIDTPDNRTRVVDNHNYYVSRVYGPCKEQSDLWDLVANRSHV 120
Qy 120 KIHTILSNTHRQASRVVLSFDFPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLM 179
Db 121 KIHRISSSHRQASRVVLSFDFPFYGHPLRQITTIATGGFIFMGDMLHRMLTATQYVAPLM 180
Qy 180 ANFNPGYSDNSTVYFDPNGTVVQWDHVYLQGWEDKGSFTFOAALHHDGRIVEAYKEIP 239
Db 181 ANFNPGYSDNSTVAIFDPNGTVVQWDHVYLQDREDRGSFTFOAALHRDGRIVEYKEIP 240
Qy 240 MSVPEISSOHVPKVTGLSDAFMILNPSDPVPESSRRSIFFEYHRIELDPKVTMSAVEFT 299
Db 241 MAVLDISSAHPVKAGLSDAFMIILNSSPEVPESQRRIFFEYHRVELDSSKITTTSAVEFT 300
Qy 300 PLPTCLQHRSCDCAWSSDLTFNCWCHVLRCCSGFDPRYQEWMDYCAQAEGRMCEDF 359
Db 301 PLPTCLQHQSCDTCVSSNLTFNCWCHVLRCCSGFDPRYQEWLTYGCAQAEAGKTCEDF 360
Qy 360 QDEHDSASDPTSPSPVDGDLTTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPTKKG 419
Db 361 QDDSHYASDPSSFPNGD-STTSSSLFIDSLTTEDDTKLNYPAGDGLPDHSSPKSKG 419
Qy 420 TPVHLGTIVGVLAVLVAAILAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHS 479
Db 420 PPVHLGTIVGVLAVLVAAILAGIYISGHPNSNAALFFIERRPHWPAMKFRSHPDHS 479
Qy 480 TYAEVPSGHEKEGFVEAEQC 500
Db 480 TYTEVEPSGHEKEGFVEAEQC 500
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Db 420 PPVHLGTIVGVLAVLVAAILAGIYISGHPNSNAALFFIERRPHWPAMKFRSHPDHS 479
Qy 480 TYAEVPSGHEKEGFVEAEQC 500
Db 480 TYTEVEPSGHEKEGFVEAEQC 500

RESULT 15
US-10-474-794-297
; Sequence 297, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Mouse
US-10-474-794-297

Query Match 82.1%; Score 2209; DB 16; Length 500;
Best Local Similarity 81.6%; Pred. No. 1.5e-202;
Matches 409; Conservative 46; Mismatches 44; Indels 2; Gaps 2;

Qy 1 MRGELWLL-VLVLRARALSPQAGHDEGPGSGWAAGTVRGWNRARSPGHVSEPD 59
Db 1 MRAQLWLLQLLLRGAARALSPATPAGHNEGQDSAWTAKTRQGSRRPRESPAQVLKPG 60
Qy 60 RTQLSQDLGGGTLAMDTPDNRTRVVDNHSYYVSRLYGPSEPHSRELWVDVAEANSQV 119
Db 61 KTQLSQDLGGGSLAIDTPDNRTRVVDNHNYYVSRVYGPCKEQSDLWDLVANRSHV 120
Qy 120 KIHTILSNTHRQASRVVLSFDFPFYGHPLRQITTIATGGFIFMGDVIHRMLTATQYVAPLM 179
Db 121 KIHRISSSHRQASRVVLSFDFPFYGHPLRQITTIATGGFIFMGDMLHRMLTATQYVAPLM 180
Qy 180 ANFNPGYSDNSTVYFDPNGTVVQWDHVYLQGWEDKGSFTFOAALHHDGRIVEAYKEIP 239
Db 181 ANFNPGYSDNSTVAIFDPNGTVVQWDHVYLQDREDRGSFTFOAALHRDGRIVEYKEIP 240
Qy 240 MSVPEISSOHVPKVTGLSDAFMILNPSDPVPESSRRSIFFEYHRIELDPKVTMSAVEFT 299
Db 241 MAVLDISSAHPVKAGLSDAFMIILNSSPEVPESQRRIFFEYHRVELDSSKITTTSAVEFT 300
Qy 300 PLPTCLQHRSCDCAWSSDLTFNCWCHVLRCCSGFDPRYQEWMDYCAQAEGRMCEDF 359
Db 301 PLPTCLQHQSCDTCVSSNLTFNCWCHVLRCCSGFDPRYQEWLTYGCAQAEAGKTCEDF 360
Qy 360 QDEHDSASDPTSPSPVDGDLTTTSSSLFIDSLTTEDDTKLNYPAGDGLQNNLSPTKKG 419
Db 361 QDDSHYASDPSSFPNGD-STTSSSLFIDSLTTEDDTKLNYPAGDGLPDHSSPKSKG 419
Qy 420 TPVHLGTIVGVLAVLVAAILAGIYINGHPTSNAAALFFIERRPHWPAMKFRSHPDHS 479
Db 420 PPVHLGTIVGVLAVLVAAILAGIYISGHPNSNAALFFIERRPHWPAMKFRSHPDHS 479
Qy 480 TYAEVPSGHEKEGFVEAEQC 500
Db 480 TYTEVEPSGHEKEGFVEAEQC 500
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Search completed: November 3, 2005, 20:54:14
Job time : 170 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 3, 2005, 20:45:35 ; Search time 41 seconds
(without alignments)
1173.375 Million cell updates/sec

Title: US-09-918-715-230
Perfect score: 2691
Sequence: 1 MRGELMLLVLRRAARALS.....YAEVPSGHEKEGFMEAEQC 500

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	611	22.7	476	T19786	hypothetical prote
2	126	4.7	1161	S31213	nidogen precursor
3	115.5	4.3	1568	T09074	semaphorin recepto
4	103.5	3.8	979	C86446	probable cellulose
5	101.5	3.8	743	T09173	EH domain protein
6	101	3.8	733	E86345	hypothetical prote
7	100	3.7	535	S18606	phosphoenolpyruvat
8	99	3.7	1133	T12529	hypothetical prote
9	98	3.6	345	T16074	hypothetical prote
10	98	3.6	1502	S45429	probable membrane
11	97	3.6	708	T83196	NEDD-4 ORF - mouse
12	96.5	3.6	397	S33415	corticosteroid-bin
13	96.5	3.6	679	T19703	hypothetical prote
14	95.5	3.5	399	S71480	homeotic protein H
15	95.5	3.5	887	S70842	ubiquitin ligase N
16	95.5	3.5	2120	T30243	alpha tectorin - c
17	94	3.5	774	JC7265	neprilysin (EC 3.4
18	93.5	3.5	979	T2349	protein-tyrosine-p
19	93.5	3.5	996	I48721	PPP 35 protein - m
20	93.5	3.5	1977	S54771	sodium channel alp
21	93	3.5	491	AG3506	phosphoenolpyruvat
22	93	3.5	1085	S55352	IRP1 protein - yea
23	92.5	3.4	441	JC7653	pectate lyase (EC
24	92.5	3.4	852	A85041	probable receptor
25	91.5	3.4	614	A98241	hypothetical prote
26	91.5	3.4	614	T F8688	hypothetical prote
27	91.5	3.4	810	P2WMBB	2a protein - broad
28	91.5	3.4	1042	A57534	mucin 5AC (clone L
29	91	3.4	633	S47144	mating type A prot

30 91 3.4 1175 2 S51005 protein-tyrosine-p
31 90.5 3.4 332 2 JN0067 pregnancy-specific
32 90.5 3.4 424 2 S70399 zona pellucida gly
33 90.5 3.4 4848 2 T30289 pristinamycin I sy
34 90 3.3 561 2 AD2581 phosphoenolpyruvat
35 90 3.3 561 2 B97363 phosphoenolpyruvat
36 90 3.3 798 2 T25104 hypothetical prote
37 90 3.3 1176 2 I58345 protein tyrosine p
38 90 3.3 1179 2 T05673 hypothetical prote
39 90 3.3 1189 2 T51491 hypothetical prote
40 90 3.3 1621 2 T30200 protein-tyrosine k
41 90 3.3 2825 2 T14271 Doc4 protein, stre
42 89.5 3.3 424 2 A34595 pregnancy-specific
43 89.5 3.3 1376 2 G00043 oateonidogen - hum
44 89.5 3.3 1762 2 T03222 probable polyketid
45 89.5 3.3 1840 1 CHRTM1 sodium channel pro

ALIGNMENTS

RESULT 1
T19786
hypothetical protein C36E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19786
R;Wilkinson, J.; Barlow, K.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19177
A;Accession: T19786
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-476 <WIL>
A;Cross-references: UNIPROT:Q18500; EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:C3
A;Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3

Query Match 22.7%; Score 611; DB 2; Length 476;
Best Local Similarity 34.2%; Pred. No. 5.6e-42;
Matches 149; Conservative 65; Mismatches 160; Indels 62; Gaps 15;
QY 46 RRARESPGHVSEPDRTQLS-----QDLGGGTAMDTLPDNRTRVVEDNHSYYSRLYGPS 100
DB 62 RTAARAP-----IPKRSLSAQEDEDIDPATATIP--PDVEVKNDMDHQYQAETFGVD 115
QY 101 EPHSRELWVDVAEANSQVKI----HTILSNTHRQASRVVLSFDFPPYGHPLRQITITATG 156
DB 116 GETLKYWINVBOFMKKPKAVGNTSHPLLSQSRRVAVGARLQKFPFYGHGMNLTITATG 175
QY 157 GFIFMGDVIHRMLTATQYVAPLMAFNPNPGYSNNTVYFDNGTVFVQVQDHRVYLQGWEDK 216
DB 176 GFYIGDHSNHLAAATQYAPLMAFNHT-YLNNSNIVYADGGLFVVEWNRVQLKEDKE 234
QY 217 GSTTFOAALHGDGRIVFAYKBIKPMSPVPEISSQHPVKVTGLSDAFMILN--PSPDVPSSRR 274
DB 235 HSFTFTILHKGNDIVFIYKDVYDISNDANHPVKLGISDAYMFKHNLHQAAPV---K 291
QY 275 RSIFFEYHRLDPSKVTSMSSAVEFTPLPCLQHRSDACMSDDLTPNCSSCHVLQR--- 330
DB 292 RVYIEYHRIEIAAQKIVSNVTWILKAQPTCISPDCTCTNATLPHFNCLWCHAKKSHGG 351
QY 331 --CS--SGFDRVQEWMDYCAQEAEGRMCE-DFQEDHDSAS-PDTSFSPYDGLTFTTS 384
DB 352 PFTCDRAGLHRRQRHWFEGNCYQRKALYCDADDEDEYDEEDYPKSQLMPNGH---TV 408
QY 385 SSLFIDSLTTEDDTKLNPYAGDGLQNNISPRTKGTGTPVHLGTTIVGIVLAVLLVAAILAG 444
DB 409 LPLDADKMKTKTTSDESDSEWKGHKKKEPK-----GG 442

QY 445 IYINGHP--TSNAALF 458
Db 443 VATTAPVGTSSQAATF 458

RESULT 2
nidogen precursor - sea squirt (Halocynthia roretzi)
N/Alternate names: entactin
C/Species: Halocynthia roretzi
C/Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C/Accession: S31213
R/Nakae, H.; Sugano, M.; Ishimori, Y.; Endo, T.; Obinata, T.
Eur. J. Biochem. 213, 11-19, 1993
A/Title: Ascidian entactin/nidogen. Implication of evolution by shuffling two kinds of c
A/Reference number: S31213; MUID:93238676; PMID:8477687
A/Accession: S31213
A/Molecule type: mRNA
A/Residues: 1-1161 <NAK>
A/Cross-references: UNIPROT:Q04901; EMBL:D14038; NID:G217363; PIDN:BAA03127.1; PID:G2173
C/Superfamily: Ascidian nidogen; EGF homology; LDL receptor WYTD-containing repeat homol
C/Keywords: basement membrane; collagen binding; disulfide bond; duplication; extracellu
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-1161/Product: nidogen #status predicted <MAT>
F/274-306/Domain: EGF homology <EG1>
F/560-574/Region: 3-residue repeats (R-P-V)
F/603-673/Domain: thyroglobulin type I repeat homology <THY1>
F/686-748/Domain: thyroglobulin type I repeat homology <THY2>
F/752-819/Domain: thyroglobulin type I repeat homology <THY3>
F/900-943/Domain: LDL receptor WYTD-containing repeat homology <YW1>
F/944-986/Domain: LDL receptor WYTD-containing repeat homology <YW2>
F/987-1031/Domain: LDL receptor WYTD-containing repeat homology <YW3>
F/1032-1075/Domain: LDL receptor WYTD-containing repeat homology <YW4>
F/1076-1114/Domain: LDL receptor WYTD-containing repeat homology <YW5>
F/1129-1158/Domain: EGF homology <EG2>
F/107,334,360,484/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 4.7%; Score 126; DB 1; Length 1161;
Best Local Similarity 23.5%; Pred. No. 0.094;
Matches 64; Conservative 34; Mismatches 88; Indels 86; Gaps 12;

QY 137 LSPDFPVGHPLRQITATGGFIEM-----GDVTHRLMTATQYVAPLMAN----- 181
Db 47 LSPDIVFYDQYDSVTVHTDGFITLNVGADTDGEVL-----LAPFMSDLDTLSG 97

QY 182 --FNPFGYSDNSTVYV-----FDNGTVFVQWDHVVYLOGWEDKGSFTFQAA 224
Db 98 DIFREHKDNATIRANTDVREAFIETAGDFNAGSVFVVTWVKQASREDGVTFTFQCI 157

QY 225 LHDGRIVFA---YKEIPMSVPEIS---SSQHPVKTKGLSDA-----PMILNPSP-----DV 269
Db 158 VATDGAATFAIFLYPDQGLAVGENAVKGVNEVTARAGFNDGGREQLLEILSADELLGGDN 217

QY 270 PESRRRIFEVHRIELDPKSVTSNAVEFTPLPCLQHRSDCADMSDDLTFNCSWCHVLQ 329
Db 218 AGSGQGWIFQIGGIMFNNDASKESK-----KH-----HVKX 249

QY 330 RCSGDFRYRQEW-MDYGCAQAEF-GRMCBDF 359
Db 250 TRQSGFQVSEWFNEDFNIDLEACGTPCSDP 281

RESULT 3
T09074
semaphorin receptor VESPR - human
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T09074
R/Comeau, M.R.; Johnson, R.; DuBoise, R.F.; Petersen, M.; Gearing, P.; van den Bos, T.; H
Immunity 8, 473-482, 1998
A/Title: A poxvirus-encoded semaphorin induces cytokine production from monocytes and b
A/Reference number: Z16555; MUID:98246049; PMID:9586637

A/Accession: T09074
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: mRNA
A/Residues: 1-1568 <COM>
A/Cross-references: UNIPROT:O60486; EMBL:AF030339; NID:G3176761; PIDN:AAC18823.1; PID:G3
A/Experimental source: tissue type foreskin; cell type fibroblast
C/Genetics:
A/Gene: VESPR
C/Keywords: receptor; signal transduction

Query Match 4.3%; Score 115.5; DB 2; Length 1568;
Best Local Similarity 20.6%; Pred. No. 1;
Matches 77; Conservative 42; Mismatches 118; Indels 137; Gaps 20;

QY 39 GTVRGMNRRARESPGHVSEPDRT-----QLSQDLGGGTFLAMDTLPDNRTRVVEDNHNHYVS 94
Db 256 GAATGWPSMAR-----IAQSTVELFQQAQLDCGHG-----PDGR-----R 292

QY 95 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHROASRVVLSF----- 139
Db 293 LLLSSSLVEALDVWAGVFSAAAGGQERRSPFTTALCLFRMSEIQARAKRVSWDFKTAES 352

QY 140 -----DPPFVGHPLRQITATGGFIEMGDVTHRLMTATQYVAPLMANFNFGYSDNSTVYV 194
Db 353 HKEGQOPERVQVIASTL-----IHSDLISV-YGTVM-----NRTVLF 391

QY 195 FDNGTVFVQWDHVVYLOGWEDKGSFTFQAAALHDGRI--VPAYKEIPMSVPEI---SSSQ 249
Db 392 LGTG-----DGQLLKVLGENLTSCNCPVETIYKEE 422

QY 250 HPVKTGLSDAFMILNPSDPVPSRRRSIFVHRIELDPKSVTSNAVEFTPLPCLQHRSS 309
Db 423 TPV-----FYKLVPDP-----VKNIIYV-----LTAGKEVRRIRVANCNKHS 460

QY 310 CDACMSDLTFNCSWCHVLQRCSSGDFRYRQE---WMDYGCAQAEGRMCEDFQ-----D 361
Db 461 CSECLTA-TDPHCGWCHSLQRCFTFGDCVHSENLENWLDI-----SSGAKKCPKIQIIRSS 515

QY 362 EDHDSASPDTSPSP 375
Db 516 KEXTVTVMGSPSP 529

RESULT 4
C86446
probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: C86446
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Hughes, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Huh, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: C86446
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-979 <STO>
A/Cross-references: UNIPROT:Q9FVR3; GB:AE005172; NID:g10801364; PIDN:AAG23436.1; GSPDB:G
C/Genetics:
A/Map position: 1

Query Match 3.8%; Score 103.5; DB 2; Length 979;
Best Local Similarity 21.2%; Pred. No. 5.2;
Matches 87; Conservative 48; Mismatches 167; Indels 109; Gaps 19;

QY 4 ELWLLVILREARALSPQAGHDSGPGSWAAKGTGVRGNRARESPGHVSEPDRTQL 63

Db 342 EKWKHWKVBEDQIKPRPAL---VAPKATWMDGT--HWPGTWAVSGPHSRGDHASV 396
Qy 64 SODL-----GGTLAMD-----TLPDNRTRVEDNHSYVSRLYGSEPHSR 105
Db 397 IOVLDPDGPDPVKGSGEGALDLEGVDILP-----MLVYSREKRPGYDHNK 446
Qy 106 ELWVDVAEANRSQVKIHTILNTHRSQASRVVLSFDFFPYGHPLRQITATGCFIFMGJVI 165
Db 447 K-----AGAMNALVRASAIMSN-----GPFILNLDCHYVNSRAF-----RDGICFMDHD 493
Qy 166 HRLMTATQY-----VAPLMAFNPGYSD-----NRTVYV-F 195
Db 494 GDRVSYVQFPQRFEGIDPFSRDYANKNTVFFDINLRALDGIQPMYVGTGCLFRRTALYGF 553
Qy 196 DNGTVFVVDHVLQWEDKSGFTFOALHHDGRIVFAYKEIPMSV---PEISSQHP- 251
Db 554 NPPDVVFE-----EESGSGYCFP-----LIRKSPATVASEPEYYTDEDR 595
Qy 252 -----VKTGLSDAFMILNPSDPVPSRRRSIFEYH--RIELDPKVT-SMSAVEFTPLPT 303
Db 596 FDIGLIRKQFGSSMLVN-SVKVAEFEGRPLATVHSSRLGPPGSLGSRKPLDFATVNE 654
Qy 304 CLQHRSCDACMSDLTNCWCH--VLQRCSSGFDYRQEMWYGCQAE 352
Db 655 AVNVISCWYEDKTEWGFNGVNGIYGVTEVDVVTGPRMEKGRSPYCVTEPD 705

RESULT 5
T09173
EH domain protein Reps1 - mouse
N;Alternate names: RalBP1-associated EH domain protein Reps1
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09173
R;Ramaguchi, A.; Urano, T.; Goi, T.; Feig, L.A.
J. Biol. Chem. 272, 31230-31234, 1997
A;Title: An eps homology (EH) domain protein that binds to the ral-GTPase target, RalBP1
A;Reference number: 216602; MUID:98058900; PMID:9395447
A;Accession: T09173
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-743 <YAM>
A;Cross-references: UNIPROT:O54916; EMBL:AF031939; NID:g2677842; PIDN:AA894736.1; PID:g2677842
A;Experimental source: cell line: C2C12; tissue type: muscle
C;Genetics:
A;Gene: rep1
C;Keywords: signal transduction

Query Match 3.8%; Score 101.5; DB 2; Length 743;
Best Local Similarity 18.3%; Pred. No. 5.1;
Matches 91; Conservative 63; Mismatches 166; Indels 177; Gaps 23;

Qy 19 LSPQPGAGH-DEGPGSGWAAK-----GTVRGWRNRARESPGHV 55
Db 78 IPPPGGRGVKGGSHDAVQPRPSAQBPSPVSPQSPPTSPHTWKRKSRHPSGGN 137
Qy 56 SEPDRITQSQ-----DLGGTLAMDPLPNRTRVEDNHSYVSRLYGSEPHSRRLW 109
Db 138 SERPLTGPFPWSPFGDAQGSSAGDAV-----WSGQSPPPQDNWV 179
Qy 110 DVAB-----ANRSQVKHTILS-NTHRQASRVVLGDFPFGYGHPLRQITAT 155
Db 180 SPADTPPTSALLTHGPASVQDQTVTRIVASAAANEIRROSSYEDPW-----KITDE- 232
Qy 156 GGFIFMGDVIHRLMTATQY--VAPLMAFNPGYSDNSTVYVFNQTVFVQWHDVY-LQG 212
Db 233 -----QROYVNVQFKTIQDNLNGFIPG---SAAKEFFTKSKLPILSLHIWELSD 279
Qy 213 WEDKGSFT---FOALHHDGRIVFAYK---EIPMSVPEISSQHPVKTGLSDAFMILNPS 266
Db 280 FDKDGAULTDFECAAFF-----LVARKNGYDLPEKLP-----SLMPKLIIDLEDS 325

Qy 267 PDVPESRRRSIFEYHRIELDPKSVTMSAVEFTPLPTCLQHRSCDACMSDLTNCWCH 326
Db 326 ADVGEQGEVGYSGSPAEPSPKSPMSL-----NQTWPE 361
Qy 327 VLQRCSSGFDYRQEMWYGCQAEAGRMCEDEFOEDHDSASPDTS----- 372
Db 362 LNOS-----SQWETFS-ERSSSQTLTQF-DSNIAPADPDTAIVHPVPIRMTFSKI 411
Qy 373 -----FSPYDGLTITSSSIFDLSLTEDDTKLPN-----YAGDGLQNNLS 414
Db 412 HMQEMELKRTSSDHTNTEPLLVPKPSLSEBENKINSSVFPNGNTVDGYSDDSPPSD-- 469
Qy 415 PKTKGTEV-----HLGT 426
Db 470 PEQIGSSVTRQSRHSGT 486

RESULT 6
E86345
hypothetical protein F16F4.9 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86345
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Huizar, L.; Jensen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E86345
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-733 <STO>
A;Cross-references: UNIPROT:Q91MN7; GB:AB005172; NID:g8920637; PIDN:AAF81359.1; GSPDB:GN C;Genetics:
A;Map position: 1
C;Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25; prot

Query Match 3.8%; Score 101; DB 2; Length 733;
Best Local Similarity 24.1%; Pred. No. 5.5;
Matches 59; Conservative 24; Mismatches 72; Indels 90; Gaps 13;

Qy 257 SDAFMILNPSDPVPSRRRSI-----FYHRIELDPKSVTMSAVE-FTPLPTCL 305
Db 139 STGMSLCDTTPPPNSKNGVGCRTVSPILDSHRIETQPSRFENNTSVEHFN----- 193
Qy 306 QHRSCD-ACMSDLTNCWCH-----WCHVLCRC-----SS 333
Db 194 -----CSYAFPEVDEGMFNFSSLEDLKLNRVTRFPVLLDWSIGNQTCRQVYVGRNCGGNST 249
Qy 334 GFDYRQEMWYGCQAEAGRM-----CEDFQD---EDHDSASPD-----SP---SPY 376
Db 250 CFPDSTGKGVNCKLQGFQDGNPYLSDCCQDINECTTRIHCSDTSTCENTILGSHCCQPS 309
Qy 377 DGLTITSSSLFSDLSLTEDDTKLPNYPAGDGLQNNLSPKTKG-TPVHLGTIVGIVLAVL 435
Db 310 GSDLNTTWSG-IDTPKEE-----PKYLGWTTVLLGTGTFLLILL 349
Qy 436 LVAAL 440
Db 350 TISYI 354

RESULT 7
S18606
phenololpyruvate carboxylase (ATP) (EC 4.1.1.49) - Rhizobium sp.
C;Species: Rhizobium sp.
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 27-Oct-2003

C;Accession: S18606
R;Osteras, M.; Finan, T.M.; Stanley, J.
Mol. Gen. Genet. 230, 257-269, 1991
A;Title: Site-directed mutagenesis and DNA sequence of pcka of Rhizobium NGR234, encoding
A;Reference number: S18606; MUID:92079905; PMID:1720862
A;Accession: S18606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-535 <OST>
A;Cross-references: EMBL:X63291
C;Superfamily: phosphoenolpyruvate carboxykinase [ATP]
C;Keywords: carbon-carbon lyase; carboxy-lyase; nucleotide binding; P-loop
P;234-241/Region: nucleotide-binding motif A (P-loop)

Query Match 3.7%; Score 100; DB 2; Length 535;
Best Local Similarity 19.8%; Pred. No. 4.3;
Matches 71; Conservative 50; Mismatches 157; Indels 80; Gaps 15;

Qy 11 VLREAAALSPQAGHDEGPGSCWAAKGTVRGWNRRARSPGHV--SEPDRTQLSQDLG 68
Db VFRPLGSLQLRAAELEYE-----AFARRGALTAHGALCARTGQHTGRSPKDKYVVRDAAT 72
Qy 69 GGTLAMDT-----LPDNRTRVVED-----NHSYVVSRLYGPSEPHSRELWVDVAEANKRSQ 118
Db 73 GDQLWWDNNSAISPENFERLRQDMLAHAKGMSLVQDLVGAGQSGK-----CVADARRHR 127
Qy 119 VKIHTI-LSNTHRQASRVLS-----FDFFP-FYGHF-----LRQITIA 154
Db 128 IRWHSLEIRNLLIRPPREGLASFLPKLTIIDLPSEKANKPERHGCGETIITACDLTKGLVL 187
Qy 155 TGGFIFMGDVIHRLMTATQYAP-----LMAFNFGYSDNSTVYF----- 195
Db 188 IGGTSYAGEMKKSFTVNLNLLPNKAVMPHCSANVGPA---GDTAIFFLSGTGKTTLS 244
Qy 196 -DNGTVFVQWDHYVLOQWEDKSGFTFOAALLHDGRIVFAYKEIPMGVPEISSSQHPVK 254
Db 245 ADPNRTILGDEH---GWSDKGVNFEG-----GCYAKAIRLSEAAPEIPATRRFGT 295
Qy 255 GLSDAFMLNPSPPVPSRRRSIFEYHRIELDPKSVTSMGAVEFTPTCLQHRSCDA 312
Db 296 VMENVLDERRAPDFDNG---SLTENTRIAYPLDFIPNASBTGTAPQPTIIMLTADA 350

RESULT 8
T12529
hypothetical protein DKFZp3434P113.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12529
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: 217524
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1133 <WAM>
A;Cross-references: UNIPROT:Q9UG37; EMBL:AL080145
A;Experimental source: adult testis; clone DKFZp3434P113
C;Genetics:
A;Note: DKFZp3434P113.1

Query Match 3.7%; Score 99; DB 2; Length 1133;
Best Local Similarity 23.0%; Pred. No. 15;
Matches 67; Conservative 37; Mismatches 119; Indels 68; Gaps 16;

Qy 162 GDVTHRLMTATQYVAPLMAFNPGYSNNTVYFDNGTVFVQWDHYVLOQ--WE----- 214
Db 823 GDIAH--IYDIQTGNKLLTFENPLANN-----YKNCATFNPTDLDVNDGLMDVRSQA 876
Qy 215 -----DKGSFTFOAALLHDGRIVFAYKEI-----PMSVPEISSSQ---HPVKTLGSD 258
Db 877 AIHKFDKFNMMISGVFHPNGLEVIINTEIMDLRTFLLHLTVPALDQCRVFNHTGTWYMG 936

Qy 259 AFMLNPSPPVPSRRRSIFEYHRIELDPKSVTSMGAVEFTPTCLQHRSCDACMSSD 317
Db 937 AMLQADDEDLMBERMKSPF-----GSSFRFTNATDYKPIATIDVKRNIPDLCTD-- 986
Qy 318 LTFNCSCHVLQRCSSGFDRYRQEWMDYGC-----AQAEAGRMCEDFQDEBDH 364
Db 987 -TKDC-YLAVIENQGS-MDALN--MDTVCRLEYVGRQRLAEDEDEDEDEDEDEDE 1040
Qy 365 DSASPDTFSFYDGDLTSTSSSLFIDSLTTFDDTKLNPYAGDGLQNNLSP 415
Db 1041 DEDDDDDTD-----DLDELDTDLQLEAELEDDN--NENAGEDG-DNDFSP 1082

RESULT 9
T16074
hypothetical protein F14B8.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16074
R;Geisel, C.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F14B8.
A;Reference number: Z18456
A;Accession: T16074
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-345 <GBI>
A;Cross-references: UNIPROT:Q19446; EMBL:U28737; NID:g860717; PID:g860723; PIDN:AAA68276
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F14B8.6
A;Introns: 17/3; 61/2; 93/3; 144/2; 197/1; 218/3; 255/2; 327/3

Query Match 3.6%; Score 98; DB 2; Length 345;
Best Local Similarity 18.7%; Pred. No. 3.4;
Matches 50; Conservative 46; Mismatches 95; Indels 76; Gaps 12;

Qy 240 MSVPETSSQHPVKTGLSDAFMLNPSPPVPSRRRSIFEYHRIELDPKSVTSMGAVEFT 299
Db 96 ISVSGIATMKCATLGNASDFFLLMTQSSNQPDNRNQN-----TPIQVTS-NTNQWT 145
Qy 300 PLPTCLQHRSCDACMSSDLTFNCSCWCHVLQRCSSGFDRYRQEWMDYGCQAEAGRMCEDF 359
Db 146 LTATI--NRKCG--ADQYGFNCN-----EQCST-----VNDYYCYTCGSGNQKTCAS- 191
Qy 360 QDEHDSDSPDTFSFYDGDLTSTSSSLFIDSLTTFDDTKLNPYAGDGLQNNLSPKTKG 419
Db 192 -----GDVNPED-DCSYVDHPISITWSP-----NTQCSASAEN 222
Qy 420 TPVHLGTIVGIVLAVLLVAAIL-----AGIY-----INGHPTSNAALFF 459
Db 223 TYFWMISFAIITAILAILLLELLVLELCCGLFTGQSRSESDGDWIVPKTKANHELVD 282
Qy 460 IERRPHHPAMKFRSHPDHSTYAEVPE 486
Db 283 ADITPHK---QYRRRHQDNNSGESTEP 306

RESULT 10
S45429
Probable membrane protein YBL079w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBL0725
C;Species: Saccharomyces cerevisiae
C;Date: 09-Jun-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: S45429; S45820; S45815; S59226
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
submitted to the EMBL Data Library, May 1994
A;Description: Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces ce
A;Reference number: S45387
A;Accession: S45429
A;Molecule type: DNA
A;Residues: 1-1502 <OBE>
A;Cross-references: UNIPROT:P38181; EMBL:X79489; NID:g496661; PID:g496702

C;Keywords: glycoprotein; steroid binding
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-397/Product: corticosteroid-binding globulin #status experimental #MAT>
F;89,169,217,232,253,320/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 3.6%; Score 96.5; DB 2; Length 397;
Best Local Similarity 20.2%; Pred. No. 5.5;
Matches 53; Conservative 47; Mismatches 104; Indels 59; Gaps 11;
Qy 61 TQLSQDLGGTGLAMDTLPDRNRTRVEDNHSYVRLYGPSEPHSRELWVDVAE-----A 114
Db 114 TGLEMMGNVFWLQLKXDSFLADTKHYVESEALTPSKD-----WTKAGEQINNHNK 168
Qy 115 NRSQVKHTILSNTHROASRVVLSDFP-----PFYGHPLRQITATGCFIFMGDVIHR 167
Db 169 NKTQKGKIEHVVDLSDSATILINIFLKGWKLFPSPENTRE-----EDFYV 216
Qy 168 MLTATQVAPLMAFNFPYSDNSVW-----YFDNGTVFVQWDHVYLQGWEDKGSFT 220
Db 217 NETSTVKPMVQSGNLSYFRDSAI PCQMVMYVNGTTFIILPD-----QGQMD-----T 268
Qy 221 FQALHHD-----GRIVFAYKEIPMSVPEISSQH-----PVKTLGLSDAFMILNPSPDV 269
Db 269 VVAALNRDITDRMCKMLP-RQNNLYIPKFSMSDTPYDLQVLDVGIKDLFTNQSDFAIT 327
Qy 270 PESRRRSIFVHR--IELDFSKV 290
Db 328 TKOTPLTLTLVHLKAMLQDEGNV 350

RESULT 13
T19703
hypothetical protein C34C12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19703
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19166
A;Accession: T19703
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-679 <WIL>
A;Cross-references: UNIPROT:Q09495; EMBL:Z46996; PIDN:CAA87102.1; GSPDB:GNO0021; CESP:C3
A;Experimental source: clone C34C12
C;Genetics:
A;Gene: CESP:C34C12.2
A;Map position: 3
A;Introns: 5/3; 72/3; 125/3; 173/3; 511/3; 605/3

Query Match 3.6%; Score 96.5; DB 2; Length 679;
Best Local Similarity 23.3%; Pred. No. 12;
Matches 70; Conservative 36; Mismatches 130; Indels 65; Gaps 12;
Qy 16 ARALSPQAGHDGPGSGWAAKTVRGWNRARSPGHVSEPDRTQLSQDLGGTGLAMD 75
Db 337 AKYLPQDPSTSSACYPKPFYESTSSSRKPIITASPQ---PPGRTQISDQLNTGEVRY- 392
Qy 76 TLPDRTRVVEDNHSYVRLYGPSEPHSRELWVDVAENRSQ---VKIHTILSNTHRQA 132
Db 393 -----VNSGKPFNFS-----SESNRNKLIPGYIKPEPRYIKPEGFTSASYKAQ 439
Qy 133 SRVVLSDFFPYGHLRQITAT-----GGFIFMGDVVHRMLTATQVAPLMAFNPNFY 186
Db 440 SEGMSSE-----LKTGSATPENSCKSAHFDMPI-----SSTPYKSHVVVESDEM 486
Qy 187 SDNSTVYVF-----DNGTVFVQWDHVYLQGWEDKGSFTFQALHHDGRIVFAYKEIPMS 241
Db 487 SSSSTIGFSEKDKONAL-----GSKQSPMDIATALHN-----IFDSKEVQSS 531
Qy 242 VPEISSSQHPVKTLGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSKVTSMSAVEFTPL 301
Db 532 SSTTGSSAPPENSKSDHF-----DMPDISSTLYSRVE--PISSSSSGSTSTSAAPVVPK 585

Qy 302 P 302
Db 586 P 586

RESULT 14
S71480
homeotic protein Hox B3 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S71480
R;Scotting, P.J.; Rex, M.
submitted to the EMBL Data Library, August 1993
A;Reference number: S71480
A;Accession: S71480
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-399 <SCO>
A;Cross-references: UNIPROT:P23682; EMBL:X74506; NID:g398704; PIDN:CAA52613.1; PID:g4433
C;Genetics:
A;Gene: Hox-B3
C;Superfamily: homeotic protein Hox B3; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;160-216/Domain: homeobox homology <HOX>

Query Match 3.5%; Score 95.5; DB 1; Length 399;
Best Local Similarity 20.5%; Pred. No. 6.7;
Matches 62; Conservative 40; Mismatches 110; Indels 91; Gaps 10;
Qy 246 SSSQHPVKTLGLSDAFMILNPSDPVPSRRRSIFEYHRIELDPKSKVTSMS-----AVEFT 299
Db 94 STSSNISPGSAKVPVRKPTSVQTP-SLTQKQIFPMMKESRQNSKQSSSPSTETCSGKT 152
Qy 300 PLPTCLQHRSCDACMSDLT-----FNCSSWCH-----VLQRCSSGDFRYRQEW-----M 343
Db 153 PGSSASKRARTATYSAQLVELEKEFHFNYLCRPRVEMANLLNLSEKQIKIWFQNRM 212
Qy 344 DYCAQAEAGRMCEDFQDEHDSASPTSFSP-----YGDLTITSSSLFIDSILT 394
Db 213 KYKDKQSKGM-----GSSSGGSPGTPGPPQMOSSAGFMNALTMSNVDAPSPS 264
Qy 395 EDDTKLNPYAGGDLGNL-----SPTKTGTPVHLGT 426
Db 265 LNKPHQYAHVNTYQNPDKALQOKYTNTAPEYDPVHLQNGVAYGTPSMQGSFVTVG- 323
Qy 427 IVGIVLAVLLVAAILAGIYINGHTSNAALFTIERRPHPWAMPKFRSHPDHSTYAEVPE 486
Db 324 -----GNVVDLSLTSGPSLYGLNLPHHQA-----NMDYSGPPQWPP 361

Qy 487 SGH 489
Db 362 SQH 364

RESULT 15
S70642
ubiquitin ligase Nedda - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S70642
R;Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.
EMBO J. 15, 2371-2380, 1996
A;Title: WW domains of Nedda bind to the proline-rich PY motifs in the epithelial Na(+)
A;Reference number: S70642; MUID:96221297; PMID:8665844
A;Accession: S70642
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-887 <STA>
A;Cross-references: UNIPROT:Q62940; EMBL:U50842; NID:g1293646; PIDN:AAB48949.1; PID:g129
C;Genetics:
A;Gene: Nedda
C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui

F;54-167/Domain: protein kinase C C2 region homology <KC2>
 F;246-283/Domain: WW repeat homology <WW1>
 F;402-439/Domain: WW repeat homology <WW2>
 F;459-496/Domain: WW repeat homology <WW3>
 F;555-881/Domain: ubiquitin-protein ligase homology <UBI>

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Best Local Similarity	19.2%	Pred. No. 20;		
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QY	14	EAARALSP-----QPCAG-----HDEGPG---SCWAAKGVTRG-----WNR	47
Db	218	DQAELEPGWVLDQPDAAATHLQHPPEPSLPPEGWEERQDVLGRYYVNHESRTTQWKR	277
QY	48	ARES-----PCHVSEPDRTQLSDGLGGTGLAMDTLPDNRTR-----VVEDNH	89
Db	278	SPEDDLTDDENGDIQLQAHGAFTRRQISEVDG-----PDNHESPENWEIVREDEN	329
QY	90	SYVSR-LYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHROASRVVLSFDFPFYGHPL	148
Db	330	TIYSGQAVQSPPSGHP-DVQVRLAE-----ELDTRLT-----MYGNPA	366
QY	149	RQITIATGGFIFMGDVIHRLMTATQYVAPLM-----ANFNPGY-----SDNSTVVFNGTV	200
Db	367	TSQPVTSNHSNRSGSSQTCIFEEQPTLPVLEPTSLPGPEWEEKQDDRCGRSYYVDHNSK	426
QY	201	FVVQWDHVLYQ-----GWEDKGSFTFQAALHHDGRIVF	233
Db	427	-TTTWSKPTWQDDPRSKI PAHLRGKTPVDSNDLGLPLPGWEER-----THTDGRVFF	477
QY	234	AYKEIPMSVPEISSQHPVKTGLSDAFMILNPSDPVPESR-RRSIFPYHRIELDPKSVTS	292
Db	478	INHNKKTQWEDPRMNVAITG-----PAEPYSRDYKRYEFPFRKLKKQ-----	522
QY	293	MSAVEFTPLTCLQHRSCDACMSDLTFNCSCWCHVLCQRCSSGFDRYRQEWMDYGCQAE	352
Db	523	-----TDIPNKFEMK-----LERANILEDVYR-IMGVCRADFLK	556
QY	353	GRMCEDFQDE---DHDSASPD-----TSFSPYDGLTTTSSSLFIDSLLTTEDDT-KLN	401
Db	557	ARLWIEFDGKGLDYGGVAREWFFLISKEMFNYYG-----LFEYSATEDNYTLQIN	608
QY	402	PYAG	405
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